

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 4, 2004, 06:44:49 ; Search time 2545 Seconds
(without alignments)
9504.270 Million cell updates/sec

Title: US-09-852-100B-1

Perfect score: 810

Sequence: 1 atgcatatttaaaagggtc.....aaacgcattatatccataa 810

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:
1: em_estba:
2: em_esthum:
3: em_estin:
4: em_estmu:
5: em_estov:
6: em_estpl:
7: em_estro:
8: em_htc:
9: gb_est1:
10: gb_est2:
11: gb_htc:
12: gb_est3:
13: gb_est4:
14: gb_est5:
15: em_estfun:
16: em_estom:
17: em_gss_hum:
18: em_gss_inv:
19: em_gss_pln:
20: em_gss_vrt:
21: em_gss_fun:
22: em_gss_mam:
23: em_gss_mus:
24: em_gss_pro:
25: em_gss_rod:
26: em_gss_phg:
27: em_gss_vrl:

28: gb_gss1:
29: gb_gss2:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query				Description
		%	Match	Length	DB	
1	673	83.1	678	12	BG702759	BG702759 602684629
2	643.8	79.5	836	12	BG723403	BG723403 602694073
3	642.8	79.4	788	14	CB996712	CB996712 AGENCOURT
4	636.4	78.6	658	12	BG709182	BG709182 602675061
5	635	78.4	982	11	BC048995	BC048995 Homo sapi
6	631.6	78.0	750	12	BI458114	BI458114 603198535
7	626.2	77.3	975	12	BI546941	BI546941 603190155
8	622.4	76.8	882	12	BI464436	BI464436 603205310
9	621.6	76.7	879	12	BI462204	BI462204 603205517
10	613.4	75.7	615	13	BQ639765	BQ639765 he20a04.y
11	606.4	74.9	772	14	CB310671	CB310671 AGENCOURT
12	606	74.8	950	12	BI562596	BI562596 603256530
13	605.4	74.7	901	12	BI596830	BI596830 603243323
14	604.4	74.6	908	12	BI596662	BI596662 603243232
15	595.4	73.5	599	9	AI923178	AI923178 wn67b10.x
16	587.4	72.5	788	14	CB229262	CB229262 AGENCOURT
17	576.8	71.2	775	14	CB311691	CB311691 AGENCOURT
18	572.4	70.7	574	9	AI680904	AI680904 tx42f05.x
19	571	70.5	961	10	BF968960	BF968960 602270156
20	556	68.6	943	13	BQ232033	BQ232033 AGENCOURT
21	555	68.5	556	9	AI479764	AI479764 tm69b04.x
22	547	67.5	547	10	BE467256	BE467256 hz63f03.x
23	534	65.9	534	10	BE467235	BE467235 hz63d03.x
24	531.2	65.6	537	9	AI580361	AI580361 tm47h02.x
25	530.8	65.5	534	10	BE328144	BE328144 ht97f11.x
26	527.4	65.1	530	9	AI674462	AI674462 wc44e01.x
27	521.4	64.4	523	12	BM698864	BM698864 UI-E-DX1-
28	516	63.7	516	10	BE348755	BE348755 ht70b01.x
29	513.8	63.4	542	12	BG700625	BG700625 602682226
30	513.4	63.4	548	9	AA772225	AA772225 ai41c01.s
31	513.4	63.4	771	13	BX108300	BX108300 BX108300
32	506	62.5	507	9	AI682204	AI682204 wa71b06.x
33	503.6	62.2	603	9	AV654663	AV654663 AV654663
34	497	61.4	498	9	AI349520	AI349520 qp72g05.x
35	495.6	61.2	526	10	BE549799	BE549799_7b38g08.x
36	494.4	61.0	506	14	CB122011	CB122011 K-EST0169
37	492.8	60.8	500	9	AI680969	AI680969 tx35h07.x
38	476	58.8	870	14	CB993944	CB993944 AGENCOURT
39	475.2	58.7	799	12	BG701162	BG701162 602680739
40	474.6	58.6	586	14	CB430834	CB430834 606754 MA
41	472.8	58.4	808	14	CB991349	CB991349 AGENCOURT
42	471.2	58.2	830	14	CB992200	CB992200 AGENCOURT
43	466.2	57.6	791	14	CA451757	CA451757 UI-M-FX0-
44	464	57.3	891	10	BF692101	BF692101 602247882
45	459.2	56.7	922	13	BQ876648	BQ876648 AGENCOURT

ALIGNMENTS

RESULT 1
BG702759

LOCUS BG702759 678 bp mRNA linear EST 07-MAY-2001

DEFINITION 602684629F1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:4817358 5',
mRNA sequence.

ACCESSION BG702759

VERSION BG702759.1 GI:13974418

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 678)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM10717 row: i column: 07
High quality sequence stop: 678.

FEATURES Location/Qualifiers

source 1. .678
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4817358"
/tissue_type="hippocampus"
/lab_host="DH10B"
/clone_lib="NIH_MGC_95"
/note="Organ: brain; Vector: pBluescriptR (modified
pBluescript KS+); Site_1: BamHI; Site_2: SalI-XbaI
(gtcgag); Oligo-dT primed using primer
5'-TTTTTTTTTTTTTTTVN-3', size-selected for average
insert size 2.5 kb and normalized to ROT 5. This is a
primary library enriched for full-length clones and
constructed using the Cap-trapper method (Carninci, in
preparation). Library constructed by M. Brownstein
(NIMH/NHGRI, National Institutes of Health). Note: this
is a NIH_MGC Library."

ORIGIN

Query Match 83.1%; Score 673; DB 12; Length 678;
Best Local Similarity 100.0%; Pred. No. 4.7e-175;
Matches 673; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	135	GCTCCTGGCGGAGGCGGAAGCGGAAGTGGCGAGAAAGTGTGGTCTCCAAGATGGCGGC	194
Db	6	GCTCCTGGCGGAGGCGGAAGCGGAAGTGGCGAGAAAGTGTGGTCTCCAAGATGGCGGC	65
Qy	195	CGCCTGGCGTCTGGTCCGTCTGCTCCGGAGGCCGTGACGCCAGACTCGTGGTGTCT	254
Db	66	CGCCTGGCGTCTGGTCCGTCTGCTCCGGAGGCCGTGACGCCAGACTCGTGGTGTCT	125
Qy	255	GTGGTCGTCTCAGTC ACTACAGGACCTGGGGCTGTTGCCACCTCCGCCGGGGCGA	314
Db	126	GTGGTCGTCTCAGTC ACTACAGGACCTGGGGCTGTTGCCACCTCCGCCGGGGCGA	185
Qy	315	GGAGTCGTTAAGTGCAGGACCTCAAAGTGGACAATATAATTGTAAAGATCCAAAAT	374
Db	186	GGAGTCGTTAAGTGCAGGACCTCAAAGTGGACAATATAATTGTAAAGATCCAAAAT	245
Qy	375	AAATGACGCTACGCAAGAACCAACAGTTAACTGTACAAACTACACAGCTCATGTTCTGTT	434
Db	246	AAATGACGCTACGCAAGAACCAACAGTTAACTGTACAAACTACACAGCTCATGTTCTGTT	305
Qy	435	TCCAGCACCCAACATAACTTGTAAAGGATTCCAGTGGCAATGAAACACATTTACTGGAA	494
Db	306	TCCAGCACCCAACATAACTTGTAAAGGATTCCAGTGGCAATGAAACACATTTACTGGAA	365
Qy	495	CGAAGTTGGTTTTCAAGCCCATACTTGCCGAAATGTAAATGGCTATTCTACAAAGT	554
Db	366	CGAAGTTGGTTTTCAAGCCCATACTTGCCGAAATGTAAATGGCTATTCTACAAAGT	425
Qy	555	GGCAGTCGATTGTCCTTTCTGGATGGTGGAGCAGATCGATTACCTTGGATA	614
Db	426	GGCAGTCGATTGTCCTTTCTGGATGGTGGAGCAGATCGATTACCTTGGATA	485
Qy	615	CCCTGCTTGGTTTGTAAAGTTTGCACTGTAGGGTTTGTGGAATTGGAGCTAAT	674
Db	486	CCCTGCTTGGTTTGTAAAGTTTGCACTGTAGGGTTTGTGGAATTGGAGCTAAT	545
Qy	675	TGATTTCATTCTTATTCATGCACTGTAGGTGGACCTTCAGATGGAAGTAGTTACATTAT	734
Db	546	TGATTTCATTCTTATTCATGCACTGTAGGTGGACCTTCAGATGGAAGTAGTTACATTAT	605
Qy	735	AGATTACTATGGAACCAGACTTACAAGACTGAGTATTACTAATGAAACATTTAGAAAAAC	794
Db	606	AGATTACTATGGAACCAGACTTACAAGACTGAGTATTACTAATGAAACATTTAGAAAAAC	665
Qy	795	GCAATTATATCCA 807	
Db	666	GCAATTATATCCA 678	

RESULT 2
BG723403

LOCUS	BG723403	836 bp	mRNA	linear	EST 08-MAY-2001
DEFINITION	602694073F1 NIH_MGC_97	Homo sapiens	cDNA clone IMAGE:4826035 5', mRNA sequence.		
ACCESSION	BG723403				
VERSION	BG723403.1	GI:14002590			

KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 836)
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
 cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
 Toshiyuki and Piero Carninci (RIKEN)
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLAM10740 row: b column: 20
 High quality sequence stop: 760.
 FEATURES Location/Qualifiers
 source 1. .836
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:4826035"
 /lab_host="DH10B"
 /clone_lib="NIH_MGC_97"
 /note="Organ: testis; Vector: pBluescriptR (modified
 pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI
 (gtgcag); Oligo-dT primed using primer
 5'-TTTTTTTTTTTTTTVN-3', size-selected for average
 insert size 2.2 kb and normalized to ROT 5. This is a
 primary library enriched for full-length clones and
 constructed using the Cap-trapper method (Carninci, in
 preparation). Library constructed by M. Brownstein
 (NIMH/NHGRI, National Institutes of Health). Note: this is
 a NIH_MGC Library."

ORIGIN

Query Match 79.5%; Score 643.8; DB 12; Length 836;
 Best Local Similarity 99.7%; Pred. No. 6.2e-167;
 Matches 645; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy	164	GCGAGAAAGTGTGGTCTCCAAGATGGCGGCCGCTGGCCGTCTGGTCGTCTGCTCCGG	223
Db	2	GCGGAAAAGTGTGGTCTCCAAGATGGCGGCCGCTGGCCGTCTGGTCGTCTGCTCCGG	61
Qy	224	AGGCCGTGACGCCAGACTCGTTGGTGTCTGGTCTCGTCACTACAGGACCCT	283
Db	62	AGGCCGTGACGCCAGACTCGTTGGTGTCTGGTCTCGTCACTACAGGACCCT	121
Qy	284	GGGGGGCTGTTGCCACCTCCGCCGGGGCGAGGAGTCGCTTAAGTGCGAGGACCTCAAAG	343
Db	122	GGGGGGCTGTTGCCACCTCCGCCGGGGCGAGGAGTCGCTTAAGTGCGAGGACCTCAAAG	181

Qy	344 TGGGACAATATTTGTAAAGATCCAAAATAAATGACGCTACGCAAGAACAGTTA 403
Db	182 TGGGACAATATTTGTAAAGATCCAAAATAAATGACGCTACGCAAGAACAGTTA 241
Qy	404 GTACAAACTACACAGCTCATGTTCTGTTCCAGCACCCAACATAACTTGTAA 463
Db	242 GTACAAACTACACAGCTCATGTTCTGTTCCAGCACCCAACATAACTTGTAA 301
Qy	464 CCAGTGGCAATGAAACACATTACTGGAACGAAGTTGGTTTTCAAGCCCATA 523
Db	302 CCAGTGGCAATGAAACACATTACTGGAACGAAGTTGGTTTTCAAGCCCATA 361
Qy	524 GCCGAAATGTAAATGGCTATTCTACAAAGTGGCAGTCGCATTGTCTTTCTGG 583
Db	362 GCCGAAATGTAAATGGCTATTCTACAAAGTGGCAGTCGCATTGTCTTTCTGG 421
Qy	584 GGTTGGGAGCAGATCGATTTACCTGGATACCCCTGCTTGGTTGGTAAAGTTG 643
Db	422 GGTTGGGAGCAGATCGATTTACCTGGATACCCCTGCTTGGTTGGTAAAGTTG 481
Qy	644 CTGTAGGGTTTGTAATTGGAGCCTAATTGATTCTATTCTATTCAATGCAGAT 703
Db	482 CTGTAGGGTTTGTAATTGGAGCCTAATTGATTCTATTCAATGCAGAT 541
Qy	704 TTGGACCTTCAGATGGAAGTAGTTACATTATAGATTACTATGGAACCAAGAC 763
Db	542 TTGGACCTTCAGATGGAAGTAGTTACATTATAGATTACTATGGAACCAAGAC 601
Qy	764 TGAGTATTACTAATGAAACATTAGAAAAACGCAATTATATCCATAA 810
Db	602 TGAGTATTACTAATGAAACATTAGAAAAACGCAATTATATCCATAA 648

RESULT 3

CB996712

LOCUS CB996712 788 bp mRNA linear EST 01-MAY-2003
 DEFINITION AGENCOURT_13627955 NIH_MGC_148 Homo sapiens cDNA clone
 IMAGE:30334410 5', mRNA sequence.
 ACCESSION CB996712
 VERSION CB996712.1 GI:30291232
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 788)
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Dr. Stefan Hansson
 cDNA Library Preparation: Michael J. Brownstein (NHGRI) with help
 and advice from Piero Carninci (RIKEN)
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: NDAM354 row: i column: 19

High quality sequence stop: 566.

FEATURES Location/Qualifiers
source 1. .788
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30334410"
/tissue_type="pre-eclamptic placenta"
/lab_host="DH10B TonA"
/clone_lib="NIH_MGC_148"
/note="Organ: placenta; Vector: pBluescriptR; Site_1:
alI-XhoI; Site_2: BamH; Library is oligo-dT primed and
directionally cloned using primer
5'-TTTTTTTTTTTTTTVN-3', size-selected for average insert
size 2.3 kb and normalized to ROT 5. This is a primary
library enriched for full-length clones and constructed
using the Cap-trapper method (Carninci, in preparation).
Library constructed by M. Brownstein (NIMH/NHGRI,
National Institutes of Health). Note: this is a NIH_MGC
Library."

ORIGIN

Query Match 79.4%; Score 642.8; DB 14; Length 788;
Best Local Similarity 99.7%; Pred. No. 1.e-166;
Matches 644; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 225 GGCCGTGACGGCCAGACTCGTTGGTGTCCCTGTGGTTCGTCTCAGTCACTACAGGACCCTG 284

84 CCCCCCTGACCCGGAGACTGCTTCCTGCTCTGCTCTGCTTTCTGCTGACTGACTAGACCGAACCTG 143

Qy 285 GGGGGCTGTTGCCACCTCCGCCGGGGCGAGGAGTCGCTTAAGTGCAGGGACCTCAAAGT 344

Db 144 GGGGGCTGTTGCCACCTCCGCCGGGGCGAGGAATCGCTTAAGTGCAGGACCTCAAAGT 203

Db 204 GGGACAATATAATTGTAAAGATCCAAAAATAAATGACGCTACGCAAGAACCGAGTTAAGTG 263

Qy 405 TACAAACTACACAGCTCATGTTCTGTTCAGCACCCAACATAACTTGTAGGATT C 464
Eh 364 TAGAACTAGAGAGCTGATCTTCTGCTCTTTGGACGCCAGATACTTGTAGGATT C 323

DB 264 TACAAACTACACAGCTCATGTTCTGTTCAGCACCCAACTTGTAAGGATTC 323

QY 465 CAGTGGCAATGAAACACATTTACTGGGAACGAAGTTGGTTTTCTAAGCCCATATCTTG 524
 Pb 324 CAGTGGCAATGAAACACATTTACTGGGAACGAAGTTGGTTTTCTAAGCCCATATCTTG 383

SET 1 CHARTS FOR HIGHLY ATTENTIVE STUDENTS SET 2 CHARTS FOR HIGHLY ATTENTIVE STUDENTS

Db 384 CCGAAATGTAATGGCTATTCTACAAAGTGGCAGTCGCATTGTCTTTTCTGGATG 443

Qy	585 GTTGGGAGCAGATCGATTACCTGGATACCCTGCTTGGTTGTAAAGTTGCAC	644
Db	444 GTTGGGAGCAGATCGATTACCTGGATACCCTGCTTGGTTGTAAAGTTGCAC	503
Qy	645 TGTAGGGTTTGTGAATTGGGAGCCTAATTGATTCATTCTATTCAATGCAGATTGT	704
Db	504 TGTAGGGTTTGTGAATTGGGAGCCTAATTGATTCATTCTATTCAATGCAGATTGT	563
Qy	705 TGGACCTTCAGATGAAAGTAGTTACATTATAGATTACTATGAAACCAGACTTACAAGACT	764
Db	564 TGGACCTTCAGATGAAAGTAGTTACATTATAGATTACTATGAAACCAGACTTACAAGACT	623
Qy	765 GAGTATTACTAATGAAACATTTAGAAAAACGCAATTATATCCATAA	810
Db	624 GAGTATTACTAATGAAACATTTAGAAAAACGCAATTGTATCCATAA	669

RESULT 4

BG709182

LOCUS BG709182 658 bp mRNA linear EST 07-MAY-2001
 DEFINITION 602675061F1 NIH_MGC_96 Homo sapiens cDNA clone IMAGE:4797782 5',
 mRNA sequence.
 ACCESSION BG709182
 VERSION BG709182.1 GI:13987263
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 658)
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
 cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
 Toshiyuki and Piero Carninci (RIKEN)
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLAM10684 row: i column: 15
 High quality sequence stop: 658.

FEATURES	Location/Qualifiers
source	1..658 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGE:4797782" /tissue_type="hypothalamus" /lab_host="DH10B" /clone_lib="NIH_MGC_96" /note="Organ: brain; Vector: pBluescriptR (modified pBluescript KS+); Site_1: BamHI; Site_2: SalI-XbaI (gtgcgag); Oligo-dT primed using primer"

5'-TTTTTTTTTTTTTVN-3', size-selected for average insert size 2.3 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 78.6%; Score 636.4; DB 12; Length 658;
Best Local Similarity 99.7%; Pred. No. 6.4e-165;
Matches 637; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 172 GTGTCGGTCTCCAAGATGGCGGCCGCCTGGCCGTCTGGTCCGTCTGCTCCGGAGGCCGTG 231
| |||||||
Db 4 GGGTCGGTCTCCAAGATGGCGGCCGCCTGGCCGTCTGGTCCGTCTGCTCCGGAGGCCGTG 63

Qy 232 ACGGCCAGACTCGTTGGTGTCCCTGTGGTCGTCTCAGTCACTACAGGACCCTGGGGGCT 291
| |||||||
Db 64 ACGGCCAGACTCGTTGGTGTCCCTGTGGTCGTCTCAGTCACTACAGGACCCTGGGGGCT 123

Qy 292 GTGCCACCTCCGCCGGGGCGAGGAGTCGCTTAAGTGCAGGACCTAAAGTGGACAA 351
| |||||||
Db 124 GTGCCACCTCCGCCGGGGCGAGGAGTCGCTTAAGTGCAGGACCTAAAGTGGACAA 183

Qy 352 TATATTGTAAAGATCCAAAATAATGACGCTACGCAAGAACCAAGTAACTGTACAAAC 411
| |||||||
Db 184 TATATTGTAAAGATCCAAAATAATGACGCTACGCAAGAACCAAGTAACTGTACAAAC 243

Qy 412 TACACAGCTCATGTTCCCTGTTTCAGCACCCAACATAACTGTAAGGATTCCAGTGGC 471
| |||||||
Db 244 TACACAGCTCATGTTCCCTGTTTCAGCACCCAACATAACTGTAAGGATTCCAGTGGC 303

Qy 472 AATGAAACACATTTACTGGAACGAAGTTGGTTTTCAAGCCCATATCTGCCGAAAT 531
| |||||||
Db 304 AATGAAACACATTTACTGGAACGAAGTTGGTTTTCAAGCCCATATCTGCCGAAAT 363

Qy 532 GTAAATGGCTATTCCCTACAAAGTGGCAGTCGCATTGTCTCTTTCTGGATGGTGGGA 591
| |||||||
Db 364 GTAAATGGCTATTCCCTACAAAGTGGCAGTCGCATTGTCTCTTTCTGGATGGTGGGA 423

Qy 592 GCAGATCGATTTACCTTGGATACCCCTGCTTGGTTGTTAAAGTTTGCACGTAGGG 651
| |||||||
Db 424 GCAGATCGATTTACCTTGGATACCCCTGCTTGGTTGTTAAAGTTTGCACGTAGGG 483

Qy 652 TTTGTGAAATTGGAGCCTAATTGATTTCATTCTATTCAATGCAGATTGGACCT 711
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Db 484 TTNGTGAAATTGGAGCCTAATTGATTTCATTCTATTCAATGCAGATTGGACCT 543

Qy 712 TCAGATGGAAGTAGTTACATTAGATTACTATGGAACCAGACTTACAAGACTGAGTATT 771
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Db 544 TCAGATGGAAGTAGTTACATTAGATTACTATGGAACCAGACTTACAAGACTGAGTATT 603

Qy 772 ACTAATGAAACATTTAGAAAAACGCAATTATATCCATAA 810
| |||||||
Db 604 ACTAATGAAACATTTAGAAAAACGCAATTATATCCATAA 642

RESULT 5
BC048995
LOCUS BC048995 982 bp mRNA linear HTC 17-DEC-2003
DEFINITION Homo sapiens beta-amyloid binding protein precursor, mRNA (cDNA
clone IMAGE:5261702).
ACCESSION BC048995
VERSION BC048995.1 GI:28981340
KEYWORDS HTC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 982)
AUTHORS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E., Schnurch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
TITLE Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
PUBMED 12477932
REFERENCE 2 (bases 1 to 982)
AUTHORS Strausberg, R.
TITLE Direct Submission
JOURNAL Submitted (17-MAR-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>
COMMENT Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shiraki Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
<http://www.systemsbiology.org>
contact: amadan@systemsbiology.org
Anup Madan, Jessica Fahey, Erin Helton, Mark Kettelman, Anuradha Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
Clone distribution: MGC clone distribution information can be found

through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAK Plate: 106 Row: h Column: 9
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 7019328
This clone has the following problem: no 5' EST match.

FEATURES Location/Qualifiers
source 1. .982
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5261702"
 /tissue_type="Brain, hippocampus"
 /clone_lib="NIH_MGC_95"
 /lab_host="DH10B"
 /note="Vector: pBluescript"

ORIGIN

Query Match 78.4%; Score 635; DB 11; Length 982;
Best Local Similarity 99.2%; Pred. No. 1.8e-164;
Matches 638; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 168 GAAAGTGTGGTCTCCAAGATGGCGCCGCCTGGCGTCTGGTCCGCTGCTCCGGAGGC 227
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Db 1 GTAAAGTGTGGTCTCCAAGATGGCGCCGCCTGGCGTCTGGTCCGCTGCTCCGGAGGC 60

Qy 228 CGTGACGCCAGACTCGTTGGTGTCTGTGGTTCGTCTCAGTCACTACAGGACCCGGGG 287
 |||||||
Db 61 CGTGACGCCAGACTCGTTGGTGTCTGTGGTTCGTCTCAGTCACTACAGGACCCGGGG 120

Qy 288 GGCTGTTGCCACCTCCGCCGGGGCGAGGAGTCGCTTAAGTGCAGGACCTCAAAGTGGG 347
 |||||||
Db 121 GGCTGTTGCCACCTCCGCCGGGGCGAGGAGTCGCTTAAGTGCAGGACCTCAAAGTGGG 180

Qy 348 ACAATATATTTGTAAAGATCCAAAATAATGACGCTACGCAAGAACAGTTAAGTGTAC 407
 |||||||
Db 181 ACAATATATTTGTAAAGATCCAAAATAATGACGCTACGCAAGAACAGTTAAGTGTAC 240

Qy 408 AAACTACACAGCTCATGTTCCGTGTTCCAGCACCCAACATAACTTGTAAAGGATTCCAG 467
 |||||
Db 241 AAACTATACAGCTCATGTTCCGTGTTCCAGCACACAAACATAACTTGTAAAGGATTCCAG 300

Qy 468 TGGCAATGAAACACATTACTGGGAACGAAGTTGGTTTTCAAGCCCATACTTGCAG 527
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Db 301 TGGCAATGAAACACATTACTGGGAACGAAGTTGGTTTTCAAGCCCATACTTGCAG 360

Qy 528 AAATGTAAATGGCTATTCCCTACAAAGTGGCAGTCGATTGCTCTTTCTGGATGGTT 587
 |||||||
Db 361 AAATGTAAATGGCTATTCCCTACAAAGTGGCAGTAGCATTGCTCTTTCTGGATGGTT 420

Qy 588 GGGAGCAGATCGATTACCTGGATACCCTGCTTGGTTGTTAAAGTTGCAGTGT 647
 |||||||
Db 421 GGGAGCAGATCGATTACCTGGATACCCTGCTTGGTTGTTAAAGTTGCAGTGT 480

Qy 648 AGGGTTTGTGGAATTGGGAGCCTAATTGATTCATTCTATTCAATGCAGATTGTTGG 707
 |||||||
Db 481 AGGGTTTGTGGAATTGGGAGCCTAATTGATTCATTCTATTCAATGCAGATTGTTGG 540

Qy 708 ACCTTCAGATGGAAGTAGTTACATTATAGATTACTATGGAACCAGACTTACAAGACTGAG 767
 |||||||
 Db 541 ACCTTCAGATGGAAGTAGTTACATTATAGATTACTAAGGAACCAGACTTACAAGACTGAG 600
 |||||||
 Qy 768 TATTACTAACATTTAGAAAAACGCAATTATCCATAA 810
 |||||||
 Db 601 TATTACTAACATTTAGAAAAACGCAATTATCCATAA 643

RESULT 6

BI458114

LOCUS BI458114 750 bp mRNA linear EST 21-AUG-2001
 DEFINITION 603198535F1 NIH_MGC_96 Homo sapiens cDNA clone IMAGE:5278064 5',
 mRNA sequence.
 ACCESSION BI458114
 VERSION BI458114.1 GI:15248770
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 750)
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgaps-r@mail.nih.gov
 Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
 cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
 Toshiyuki and Piero Carninci (RIKEN)
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLAM11702 row: e column: 09
 High quality sequence stop: 711.
 FEATURES Location/Qualifiers
 source 1..750
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5278064"
 /tissue_type="hypothalamus"
 /lab_host="DH10B"
 /clone_lib="NIH_MGC_96"
 /note="Organ:-brain; Vector:-pBluescriptR_(modified
 pBluescript KS+); Site_1: BamHI; Site_2: SalI-XbaI
 (gtcgag); Oligo-dT primed using primer
 5'-TTTTTTTTTTTTTVN-3', size-selected for average
 insert size 2.3 kb and normalized to ROT 5. This is a
 primary library enriched for full-length clones and
 constructed using the Cap-trapper method (Carninci, in
 preparation). Library constructed by M. Brownstein
 (NIMH/NHGRI, National Institutes of Health). Note: this is
 a NIH_MGC Library."

ORIGIN

RESULT 7

BI546941

LOCUS BI546941 975 bp mRNA linear EST 05-SEP-2001
DEFINITION 603190155F1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:5261748 5',
mRNA sequence.
ACCESSION BI546941
VERSION BI546941.1 GI:15434253

KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 975)
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapsbs-r@mail.nih.gov
 Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
 cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
 Toshiyuki and Piero Carninci (RIKEN)
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLAM11659 row: m column: 13
 High quality sequence stop: 766.
 FEATURES Location/Qualifiers
 source 1. .975
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5261748"
 /tissue_type="hippocampus"
 /lab_host="DH10B"
 /clone_lib="NIH_MGC_95"
 /note="Organ: brain; Vector: pBluescriptR (modified
 pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI
 (gtgcag); Oligo-dT primed using primer
 5'-TTTTTTTTTTTTTTVN-3', size-selected for average
 insert size 2.5 kb and normalized to ROT 5. This is a
 primary library enriched for full-length clones and
 constructed using the Cap-trapper method (Carninci, in
 preparation). Library constructed by M. Brownstein
 (NIMH/NHGRI, National Institutes of Health). Note: this
 is a NIH_MGC Library."

ORIGIN

Query Match 77.3%; Score 626.2; DB 12; Length 975;
 Best Local Similarity 98.6%; Pred. No. 4.9e-162;
 Matches 642; Conservative 0; Mismatches 8; Indels 1; Gaps 1;

Qy	160 AGTGGCGAGAAAGTGTGGTCTCCAAGATGGCGGCCGCTGGCGTCTGGTCCGTCTGCT 219
Db	1 AGCGTGGAGTAAGTGTGGTCTCCAAGATGGCGGCCGCTGGCGTCTGGTCCGTCTGCT 60
Qy	220 CCGGAGGCCGTGACGCCAGACTCGTTGGTGCCTGTGGTCGTCTAGTCACTACAGGA 279
Db	61 CCGGAGGCCGTGACGCCAGACTCGTTGGTGCCTGTGGTCGTCTAGTCACTACAGGA 120
Qy	280 CCCTGGGGGCTGTTGCCACCTCCGCCGGGGCGAGGAGTCGCTTAAGTGCGAGGACCTC 339
Db	121 CCCTGGGGGCTGTTGCCACCTCCGCCGGGGCGAGGAGTCGCTTAAGTGCGAGGACCTC 180

Qy 340 AAAGTGGGACAATATTTGTAAAGATCCAAAATAATGACGCTACGCAAGAACCGAGTT 399
 |||||||
 Db 181 AAAGTGGGACAATATTTGTAAAGATCCAAAATAATGACGCTACGCAAGAACCGAGTT 240
 |||||||
 Qy 400 AACTGTACAAACTACACAGCTCATGTTCTGTTCCAGCACCAACATAACTTGTAAG 459
 |||||||
 Db 241 AACTGTACAAACTATACAGCTCATGTTCTGTTCCAGCACACAACATAACTTGTAAG 300
 |||||||
 Qy 460 GATTCCAGTGGCAATGAAACACATTTACTGGAACGAAGTGGTTTTCAAGCCCATA 519
 |||||||
 Db 301 GATTCCAGTGGCAATGAAACACATTTACTGGAACGAAGTGGTTTTCAAGCCCATA 360
 |||||||
 Qy 520 TCTTGCGAAATGTAAATGGCTATTCTACAAAGTGGCAGTCGCATTGTCTTTTCTT 579
 |||||||
 Db 361 TCTTGCGAAATGTAAATGGCTATTCTACAAAGTGGCAGTAGCATTGTCTTTTCTT 420
 |||||||
 Qy 580 GGATGGTTGGGAGCAGATCGATTTACCTTGGATACCCCTGCTTGGTTGTTAAAGTTT 639
 |||||||
 Db 421 GGATGGTTGGGAGCAGATCGATTTACCTTGGATACCCCTGCTTGGTTGTTAAAGTTT 480
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 Qy 640 TGCACTGTAGGGTTTGTGAATTGGGAGCCTAATTGATTCATTCTTATTCAATGCAG 699
 |||||||
 Db 481 TGCACTGTAGGGTTTGTGAATTGGGAGCCTAATTGATTCATTCTTATTCAATGCAG 540
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 Qy 700 ATTGTTGGACCTTCAGATGAAAGTAGTTACATTATAGATTACTATGAAACCAGACTTACA 759
 |||||||
 Db 541 ATTGTTGGACCTTCAGATGAAAGTAGTTACATTATAGATTACTAAGGAACCAGACTTACA 600
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 Qy 760 AGACTGAGTATTACTAATGAAACATTAGAAAAACGCAATTATATCCATAA 810
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 Db 601 AGACTGAGTATTACTAATGAAACA-TTAGAAAAACGCAATTATATCCATAA 650

RESULT 8

BI464436

LOCUS BI464436 882 bp mRNA linear EST 21-AUG-2001
 DEFINITION 603205310F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:5271098 5',
 mRNA sequence.
 ACCESSION BI464436
 VERSION BI464436.1 GI:15255092
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 882)
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
 cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
 Toshiyuki and Piero Carninci (RIKEN)
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>
Plate: LLAM11684 row: c column: 03
High quality sequence stop: 759.

ORIGIN

Query Match 76.8%; Score 622.4; DB 12; Length 882;
 Best Local Similarity 99.5%; Pred. No. 5.4e-161;
 Matches 645; Conservative 0; Mismatches 1; Indels 2; Gaps 2;

Qy 164 GCGAGAAAGTGTGGTCTCCAAGATGGCGGCCCTGGCGTCTGGTCGCTGTCCGG 223
| :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Pr 4 GGGAGAAAGTGTGGTCTCCAAGATGGCGGCCCTGGCGTCTGGTCGCTGTCCGG 63

Qy 224 AGGCCGTGACGGCCAGACTCGTTGGTGTCTGTGGTCGTCTCAGTCACTA
283
D1 61 AGGCCGTGACGGCCAGACTCGTTGGTGTCTGTGGTCGTCTCAGTCACTA
123

Qy 344 TGGGACAATATATTGTAAAGATCCAAAATAATGACGCTACGCAAGAACCGAGTTA 403
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 184 TGGGACAATATATTGTAAAGATCCAAAATAATGACGCTACGCAAGAACCGAGTTA 243

Qy 404 GTACAAACTACACAGCTCATGTTCTGTCTTCCAGCACCCAACATAACTTGTAAGGATT 463
Dy 344 CTACAAACTACACAGCTCATGTTCTGTCTTCCAGCACCCAACATAACTTGTAAGGATT 303

Qy 464 CCAGTGGCAATGAAACACATTACTGGAACGAAGTTGGTTTCAAGCCATATCTT 523
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 524 CGCGAAATGTAAATGGCTATTCCCTACAAAGTGGCAGTCGATTGTCTCTTTTCTGGAT 583

364 GCCGAAATGTAAATGGCTATTCCCTACAAAGTGGCAGTCGCATTGTCTCTTTCTGGAT 423

Qy	584 GGTTGGGAGCAGATCGATTACCTGGATACCTGCTTGGTTGTTAAAGTTTGCA	643
Db	424 GGTTGGGAGCAGATCGATTACCTGGATACCTGCTTGGTTGTTAAAGTTTGCA	483
Qy	644 CTGTAGGGTTTGTGGAATTGGGAGCCTAATTGATTCATTCTATTCAATGCAGATTG	703
Db	484 CTGTAGGG-TTGTGGAATTGGGAGCCTAATTGATTCATTCTATTCAATGCAGATTG	542
Qy	704 TTGGACCTTCAGATGGAAGTAGTTACATTATAGATTACTATGGAACCAGACTACAAGAC	763
Db	543 TTGGACCTTCAGATGGAAGTAGTTACATTATAGATTACTATGGAACCAGACTACAAGAC	602
Qy	764 TGAGTATTACTAATGAAACA-TTTAGAAAAACGCAATTATATCCATAA	810
Db	603 TGAGTATTACTAATGAAACATTAGAAAAACGCAATTATATCCATAA	650

RESULT 9

BI462204

LOCUS BI462204 879 bp mRNA linear EST 21-AUG-2001
 DEFINITION 603205517F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:5271077 5',
 mRNA sequence.
 ACCESSION BI462204
 VERSION BI462204.1 GI:15252860
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 879)
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
 cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
 Toshiyuki and Piero Carninci (RIKEN)
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLAM11684 row: b column: 06
 High quality sequence stop: 753.

FEATURES	Location/Qualifiers
source	1..879 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGE:5271077" /lab_host="DH10B" /clone_lib="NIH_MGC_97" /note="Organ: testis; Vector: pBluescriptR (modified pBluescript KS+); Site_1: BamHI; Site_2: SalI-XbaI (gtcgag); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTVN-3', size-selected for average"

insert size 2.2 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library."

ORIGIN

Query Match	76.7%	Score	621.6	DB	12	Length	879
Best Local Similarity	98.5%	Pred.	No.	8.9e-161			
Matches	638	Conservative	0	Mismatches	9	Indels	1
Gaps	1						

Qy 164 GCGAGAAAGTGTCTGGTCTCCAAGATGGCGGCCCTGGCGTCTGGTCCGTCTGCTCCGG 223
| |||||||
Db 4 GGGAGAAAGTGTCTGGTCTCCAAGATGGCGGCCCTGGCGTCTGGTCCGTCTGCTCCGG 63

Qy 224 AGGCCGTGACGGCCAGACTCGTTGGTGTCCCTGTGGTTCTCAGTCAGTCACTACAGGACCT 283
| |||||||
Db 64 AGGCCGTGACGGCCAGACTCGTTGGTGTCCCTGTGGTTCTCAGTCAGTCACTACAGGACCT 123

Qy 284 GGGGGCTGTTGCCACCTCCGCCGGGGCGAGGAGTCGCTTAAGTGCAGGACCTCAAAG 343
| |||||||
Db 124 GGGGGCTGTTGCCACCTCCGCCGGGGCGAGGAGTCGCTTAAGTGCAGGACCTCAAAG 183

Qy 344 TGGGACAATATTTGTAAAGATCCAAAATAATGACGCTACGCAAGAACAGTTA 403
| |||||||
Db 184 TGGGACAATATTTGTAAAGATCCAAAATAATGACGCTACGCAAGAACAGTTA 243

Qy 404 GTACAAACTACACAGCTCATGTTCTGTTCCAGCACCCAACATAACTTGTAAAGGATT 463
| |||||||
Db 244 GTACAAACTACACAGCTCATGTTCTGTTCCAGCACCCAACATAACTTGTAAAGGATT 303

Qy 464 CCAGTGGCAATGAAACACATTTACTGGAACGAAGTTGGTTTTCAAGCCCATATCTT 523
| |||||||
Db 304 CCAGTGGCAATGAAACACATTTACTGGAACGAAGTTGGTTTTCAAGCCCATATCTT 363

Qy 524 GCCGAAATGTAAATGGCTATTCCCTACAAAGTGGCAGTCGATTGTCTTTTCTGGAT 583
| |||||||
Db 364 GCCGAAATGTAAATGGCTATTCCCTACAAAGTGGCAGTCGATTGTCTTTTCTGGAT 423

Qy 584 GGTTGGAGCAGATCGATTTACCTGGATACCCCTGCTTGGTTAAAGTTTGCA 643
| |||||||
Db 424 GGTTGGAGCAGATCGATTTACCTGGATACCCCTGCTTGGTTAAAGTTTGCA 483

Qy 644 CTGTAGGGTTTGTGAATTGGAGCCTAATTGATTTCATTCTTATTCAATGCAGATTG 703
| |||||||
Db 484 CTGTAGGGTTCTGTGAATTGGAGCCTAATTGATTTCATTCTTATTCAATGCAGATTG 543

Qy 704 TTGGACCTTCAGATGGAAGTAGTTACATTATAGATTACTATGGAACCAGACTACAAGAC 763
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Db 544 TTGGACCTTCAGATGGAAGTAGTTACCTTATAGATTACTATGGAACCAGACTACAAGAC 603

Qy 764 TGAGTATTACTAATGAAA-CATTTAGAAAAACGCAATTATATCCATAA 810
| |||||||
Db 604 TGAGTATTACTAATGAAACCATTAGAAAAACGCAATTATATCCATAA 651

RESULT 10
BQ639765
LOCUS BQ639765 615 bp mRNA linear EST 15-JUL-2002
DEFINITION he20a04.y1 Human Retina cDNA (Un-normalized, unamplified): hd/he
Homo sapiens cDNA clone he20a04 5', mRNA sequence.
ACCESSION BQ639765
VERSION BQ639765.1 GI:21764224
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 615)
AUTHORS Wistow,G., Bernstein,S.L., Wyatt,M.K., Ray,S., Behal,A.,
Touchman,J.W., Bouffard,G., Smith,D. and Peterson,K.
TITLE Expressed sequence tag analysis of human retina for the NEIBank
Project: Retbindin, an abundant, novel retinal cDNA and alternative
splicing of other retina-preferred gene transcripts
JOURNAL Mol. Vis. 8 (4), 196-204 (2002)
MEDLINE 22103461
PUBMED 12107411
COMMENT Contact: Wistow G
Section on Molecular Structure and Function
National Eye Institute
6/331, NIH, Bethesda, MD 20892-2740, USA
Tel: 301 402 3452
Fax: 301 496 0078
Email: graeme@helix.nih.gov
Plate: 20 row: a column: 04
Seq primer: M13RP1 reverse primer (ABI).
FEATURES Location/Qualifiers
source 1. .615
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="he20a04"
/tissue_type="Retina"
/dev_stage="Adult"
/lab_host="EMDH10B"
/clone_lib="Human Retina cDNA (Un-normalized,
unamplified): hd/he"
/note="Organ: Eye; Vector: pSPORT1; Neural retina tissue
was dissected from two 80 year old donors with no observed
eye disease. 100ug of total RNA was used for library
construction. A directionally cloned cDNA library in the
pSPORT1 vector (Life Technologies) was constructed at
Bioserve Biotechnology (Laurel MD)—essentially following
the protocols of the SuperScript Plasmid System full
details of which are contained in the manufacturer's
Instruction manual (<http://www.lifetech.com/>). First
strand synthesis was carried out using a Not I
primer-adapter
[5'-pGACTAGTTCTAGATCGCGAGCGGCCCGCC(T)15-3']. EST analysis
was performed on the unamplified library at the NIH
Intramural Sequencing Center (NISC)."
ORIGIN

Query Match 75.7%; Score 613.4; DB 13; Length 615;
 Best Local Similarity 99.8%; Pred. No. 1.5e-158;
 Matches 614; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	193	GCCGCCTGGCGTCTGGTCCGTCTGCTCCGGAGGCCGTGACGGCCAGACTCGTTGGTGTC	252
Db	1	GCCGCCTGGCGTCTGGTCCGTCTGCTCCGGAGGCCGTGACGGCCAGACTCGTTGGTGTC	60
Qy	253	CTGTGGTCGTCTCAGTCACTACAGGACCTGGGGCTGTTGCCACCTCCGCCGGGGC	312
Db	61	CTGTGGTCGTCTCAGTCACTACAGGACCTGGGGCTGTTGCCACCTCCGCCGGGGC	120
Qy	313	GAGGAGTCGCTTAAGTGCAGGACCTCAAAGTGGACAATATATTGTAAAGATCCAAA	372
Db	121	GAGGAGTCGCTTAAGTGCAGGACCTCAAAGTGGACAATATATTGTAAAGATCCAAA	180
Qy	373	ATAAAATGACGCTACGCAAGAACCAAGTTAAGTACAAACTACACAGCTCATGTTCCGT	432
Db	181	ATAAAATGACGCTACGCAAGAACCAAGTTAAGTACAAACTACACAGCTCATGTTCCGT	240
Qy	433	TTTCCAGCACCCAACATAACTGTAAAGGATTCCAGTGGCAATGAAACACATTTACTGG	492
Db	241	TTTCCAGCACCCAACATAACTGTAAAGGATTCCAGTGGCAATGAAACACATTTACTGG	300
Qy	493	AACGAAGTTGGTTTTCAAGCCCATACTTGTAAAGGATTCCAGTGGCAATGAAATGGCTATTCC	552
Db	301	AACGAAGTTGGTTTTCAAGCCCATACTTGTAAAGGATTCCAGTGGCAATGAAATGGCTATTCC	360
Qy	553	GTGGCAGTCGATTGTCTCTTTCTTGGATGGTGGAGCAGATCGATTACCTTGG	612
Db	361	GTGGCAGTCGATTGTCTCTTTCTTGGATGGTGGAGCAGATCGATTACCTTGG	420
Qy	613	TACCTGCTTGGTTGTAAAGTTGCAGTTGGTGGAGCAGATGGAAATTGGAGCCTA	672
Db	421	TACCTGCTTGGTTGTAAAGTTGCAGTTGGTGGAGCAGATGGAAATTGGAGCCTA	480
Qy	673	ATTGATTCATTCTATTCAATGCAGATTGGACCTCAGATGGAAGTAGTTACATT	732
Db	481	ATTGATTCATTCTATTCAATGCAGATTGGACCTCAGATGGAAGTAGTTACATT	540
Qy	733	ATAGATTACTATGGAACAGACTTACAAGACTGAGTATTACTAATGAAACATTAGAAA	792
Db	541	ATAGATTACTATGGAACAGACTTACAAGACTGAGTATTACTAATGAAACATTAGAAA	600
Qy	793	ACGCAATTATATCCA 807	
Db	601	ACGCAATTATATCCA 615	

RESULT 11

CB310671

LOCUS CB310671 772 bp mRNA linear EST 04-MAR-2003
 DEFINITION AGENCOURT_11828318 NICHD_Rh_Ov1 Macaca mulatta cDNA clone
 IMAGE:6895132 5', mRNA sequence.
 ACCESSION CB310671
 VERSION CB310671.1 GI:28833385
 KEYWORDS EST.

SOURCE Macaca mulatta (rhesus monkey)
 ORGANISM Macaca mulatta
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
 Cercopithecinae; Macaca.
 REFERENCE 1 (bases 1 to 772)
 AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Dr. Eliot Spindel
 cDNA Library Preparation: CLONTECH
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLCM3162 row: c column: 03
 High quality sequence stop: 646.
 FEATURES Location/Qualifiers
 source 1. .772
 /organism="Macaca mulatta"
 /mol_type="mRNA"
 /db_xref="taxon:9544"
 /clone="IMAGE:6895132"
 /tissue_type="Ovary"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NICHD_Rh_Ovl"
 /note="Organ: ovary; Vector: pDNR-LIB; Site_1: Sfi I;
 Site_2: Sfi I; Cloned unidirectionally. Primer: Oligo dT.
 Average insert size 1.0-4.0 kb. Tissue pooled from
 pre-pubertal, post pubertal sn menopausal monkeys.
 Constructed by Clontech. Note: this is a NICHD Library."

ORIGIN

```

Query Match           74.9%;  Score 606.4;  DB 14;  Length 772;
Best Local Similarity 96.0%;  Pred. No. 1.4e-156;
Matches 622;  Conservative 0;  Mismatches 26;  Indels 0;  Gaps 0;

y          163 GGCAGAGAAAGTGTGGTCTCCAAGATGGCGGCCGCTGGCGTCTGGTCCGTCTGCTCCG 222
b                  || | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
y          1 GGGAGGGAAGTGTGGTCTCCAAGATGGCGGCCGCGTGGCGTCAGGTTCGTCTGCTCCG 60
b
y          223 GAGGCCGTGACGGCCAGACTCGTTGGTGTCCGTGGTCTCAGTCACTACAGGACCC 282
b                  || | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
y          61 GAGGCCGCGACTGCTAGACTCCTCGGTGTCCGTGGTCTCAGTCACTACAGGACCC 120
b
y          283 TGGGGGGCTGTTGCCACCTCCGCCGGGGCGAGGAGTCGCTTAAGTGCAGGACCTCAAA 342
b                  || | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
y          121 TGGGGGGCTGTTGCCACCTCTGCCGGGGCGAGGAGTCGCTTAAGTGCAGGACCTCAAA 180
b
y          343 GTGGGACAATATATTGTAAAGATCCAAAATAATGACGCTACGCAAGAACAGTTAAC 402
b                  || | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
y          181 GTGGGACAATATATTGTAAAGATCCAAAATAATGATGCTACGCAAGAACAGTTAAC 240
b

```

Qy	403	TGTACAAACTACACAGCTCATGTTCCAGCACCAACATAACTTGTAGGAT	462
Db	241	TGTACAAACTACACAGCTCATGTTCCAGCACCTAACATAACTTGTAGGAT	300
Qy	463	TCCAGTGGCAATGAAACACATTTACTGGAACGAAGTGGTTTCAAGCCATATCT	522
Db	301	TCCAGTGGCAATGAAACACATTTACTGGAACGAAGTGGTTTCAAGCCATATCT	360
Qy	523	TGCCGAAATGTAAATGGCTATTCTACAAAGTGGCAGTCGCATTGTCTCTTTCTTGGA	582
Db	361	TGCCGAAATGTAAATGGCTATTCTACAAAGTGGCAGTCGCATTGTCTCTTTCTTGGA	420
Qy	583	TGGTTGGGAGCAGATCGATTACCTTGATACCCTGCTTGGTTGTTAAAGTTTGC	642
Db	421	TGGTTGGGAGCAGATCGATTACCTGGATACCCTGCCTGGTTGTTAAAGTTTGC	480
Qy	643	ACTGTAGGGTTTGTGGAATTGGGAGCCTAATTGATTCATTCTATTCAATGCAGATT	702
Db	481	ACTGTAGGATTGTGGAATTGGGAGCCTAATTGATTCATTCTATTCAATGCAGATT	540
Qy	703	GTTGGACCTTCAGATGGAAGTAGTTACATTATAGATTACTATGGAACCAGACTACAAGA	762
Db	541	GTTGGACCTTCAGATGGAAGTAGTTACATCATAGATTACTATGGAACCAGACTGACAAGA	600
Qy	763	CTGACTTACTAATGAAACATTAGAAAAACGCAATTATATCCATAA	810
Db	601	CTAAGTATTACTAATGAAACATATAGAAAAACGCAATTATATCCATAA	648

RESULT 12

BI562596

LOCUS BI562596 950 bp mRNA linear EST 05-SEP-2001
 DEFINITION 603256530F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:5298943 5',
 mRNA sequence.
 ACCESSION BI562596
 VERSION BI562596.1 GI:15449910
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 950)
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
 cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
 Toshiyuki and Piero Carninci (RIKEN)
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLAM11756 row: k column: 08
 High quality sequence stop: 753.

FEATURES **Location/Qualifiers**
source
 1. .950
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5298943"
 /lab_host="DH10B"
 /clone_lib="NIH_MGC_97"
 /note="Organ: testis; Vector: pBluescriptR (modified pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcgag); Oligo-dT primed using primer 5'-TTTTTTTTTTTTVN-3', size-selected for average insert size 2.2 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 74.8%; Score 606; DB 12; Length 950;
 Best Local Similarity 98.6%; Pred. No. 1.9e-156;
 Matches 643; Conservative 0; Mismatches 5; Indels 4; Gaps 3;

Qy	161	GTGGCGAGAAAGTGTGGTCTCCAAGATGGCGGCCCTGGCGTCTGGTCCGTGCTC	220
		
Db	4	GGGGCGTGAAAGTGTGGTCTCCAAGATGGCGGCCCTGGCGTCTGGTCCGTGCTC	63
Qy	221	CGGAGGCCGTGACGCCAGACTCGTTGGTGCCTGTGGTCGTCACTACAGGAC	280
		
Db	64	CGGAGGCCGTGACGCCAGACTCGTTGGTGCCTGTGGTCGTCACTACAGGAC	123
Qy	281	CCTGGGGGGCTGTTGCCACCTCCGCCGGGGCGAGGAGTCGCTTAAGTGCAGGACCTCA	340
		
Db	124	CCTGGGGGGCTGTTGCCACCTCCGCCGGGGCGAGGAGTCGCTTAAGTGCAGGACCTCA	183
Qy	341	AAGTGGGACAATATATTGTAAAGATCCAAAATAATGACGCTACGCAAGAACAGTTA	400
		
Db	184	AAGTGGGACAATATATTGTAAAGATCCAAAATAATGACGCTACGCAAGAACAGTTA	243
Qy	401	ACTGTACAAACTACACAGCTCATGTTCTGTTCCAGCACCCACATAACTGTAGG	460
		
Db	244	ACTGTACAAACTACACAGCTCATGTTCTGTTCCAGCACCCACATAACTGTAGG	303
Qy	461	ATTCCAGTGGCAATGAAACACATTACTGGGAACGAAGTTGGTTTTCAAGCCCATAT	520
		
Db	304	ATTCCAGTGGCAATGAAACACATTACTGGGAACGAAGTTGGTTTTCAAGCCCATAT	363
Qy	521	CTTGCAGAAATGTAAATGGCTATTCTACAAAGTGGCAGTCGCATTGTCTCTTTCTTG	580
		
Db	364	CTTGCAGAAATGTAAATGGCTATTCTACAAAGTGGCAGTCGCATTGTCTCTTTCTTG	423
Qy	581	GATGGTTGGGAGCAGATCGATTACCTGGATACCCTGCTTGGTTGTTAAAGTTT	640
		
Db	424	GATGGTTGGGAGCAGATCGATTACCTGGATACCCTGC-TTGGTTGTTAAAGTTT	482
Qy	641	GCACTGTAGGGTTTGTGGAATTGGGAGCCTAATTGATTCATTCTATTCAATGCA--	698

Db	483	GCACGTAGGG-TTGTGGAATTGGGAGCCTAATTGATTCATTCTTATTCAATGCAAG	541
Qy	699	GATTGGTGGACCTTCAGATGGAAGTAGTTACATTATAGATTACTATGGAACCAGACTAC	758
Db	542	ATTGGTGGACCTTCAGATGGAAGTAGTTACATTATAGATTACTATGGAACCAGACTAC	601
Qy	759	AAGACTGAGTATTACTAATGAAACATTAGAAAAACGCAATTATATCCATAA	810
Db	602	AAGACTGAGTATTACTAATGAAACATTAGAAAAACGCAATTATATCCATAA	653

RESULT 13

BI596830
 LOCUS BI596830 901 bp mRNA linear EST 07-SEP-2001
 DEFINITION 603243323F1 NIH_MGC_96 Homo sapiens cDNA clone IMAGE:5285933 5',
 mRNA sequence.
 ACCESSION BI596830
 VERSION BI596830.1 GI:15489769
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 901)
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
 cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
 Toshiyuki and Piero Carninci (RIKEN)
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLAM11722 row: m column: 06
 High quality sequence stop: 760.
 FEATURES Location/Qualifiers
 source 1. .901
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5285933"
 /tissue_type="hypothalamus"
 /lab_host="DH10B"
 /clone_lib="NIH_MGC_96"
 /note="Organ: brain; Vector: pBluescriptR (modified
 pBluescript KS+); Site_1: BamHI; Site_2: SalI-XbaI
 (gtcgag); Oligo-dT primed using primer
 5'-TTTTTTTTTTTTTTVN-3', size-selected for average
 insert size 2.3 kb and normalized to ROT 5. This is a
 primary library enriched for full-length clones and
 constructed using the Cap-trapper method (Carninci, in
 preparation). Library constructed by M. Brownstein"

(NIMH/NHGRI, National Institutes of Health). Note: this is
a NIH_MGC Library."

ORIGIN

Query Match 74.7%; Score 605.4; DB 12; Length 901;
Best Local Similarity 98.7%; Pred. No. 2.8e-156;
Matches 631; Conservative 0; Mismatches 6; Indels 2; Gaps 2;

Qy 172 GTGTCGGTCTCCAAGATGGCGGCCGCTGGCCGTCTGGTCCGTCTGCTCCGGAGGCCGTG 231
| |||||||
Db 4 GGGTCGGTCTCCAAGATGGCGACGCTTGGCCGTCTGGTCCGTCTGCTCCGGAGGCCGTG 63

Qy 232 ACGGCCAGACTCGTTGGTGCCTGTGGTCAGTCAGTCAGGACCTGGGGGCT 291
| |||||
Db 64 ACGG-CAGACTCGTTGGTGCCTGTGGTCAGTCAGTCAGGACCTGGGGGCT 122

Qy 292 GTTGCACCTCCGCCGGGGCGAGGAGTCGCTTAAGTGCAGGACCTAAAGTGGACAA 351
| |||||
Db 123 GTTGCACCTCCGCCGGGGCGAGGAGTCGCTTAAGTGCAGGACCTAAAGTGGACAA 182

Qy 352 TATATTGTAAAGATCCAAAATAAATGACGCTACGCAAGAACAGTAACTGTACAAAC 411
| |||||
Db 183 TATATTGTCAAGATCCAAAATAAATGACGCTACGCAAGAACAGTAACTGTACAAAC 242

Qy 412 TACACAGCTCATGTTCCGTGTTCCAGCACCCAACATAACTGTAAAGGATTCCAGTGGC 471
| |||||
Db 243 TACACAGCTCATGTTCCGTGTTCCAGCACCCAACATAACTGTAAAGGATTCCAGTGGC 302

Qy 472 AATGAAACACATTTACTGGAACGAAGTTGGTTTTCAAGCCCATATCTGCCGAAAT 531
| |||||
Db 303 AATGAAACACATTTACTGGAACGAAGTTGGTTTTCAAGCCCATATCTGCCGAAAT 362

Qy 532 GTAAATGGCTATTCCCTACAAAGTGGCAGTCGATTGTCTCTTTCTGGATGGTGGGA 591
| |||||
Db 363 GGTAATGGCTATTCCCTACAAAGTGGCAGTCGATTGTCTCTTTCTGGATGGTGGGA 422

Qy 592 GCAGATCGATTTACCTGGATACCCCTGCTTGGTTGTTAAAGTTGCACTGTAGGG 651
| |||||
Db 423 GCAGATCGATTTACCTGGATACCCCTGCTTGGTTGTTAAAGTTGCACTGTAGGG 482

Qy 652 TTTGTGGAATTGGGAGCCTAATTGATTCATTCTATTCAATGCAGATTGGACCT 711
| |||||
Db 483 -TTTGTGGAATTGGGAGCCTAATTGATTCATTCTATTCAATGCAGATTGGACCT 541

Qy 712 TCAGATGGAAGTAGTTACATTATAGATTACTATGGAACCAGACTTACAAGACTGAGTATT 771
| |||||
Db 542 TCAGATGGAAGTAGTTACATTATAGATTACTATGGAACCAGACTTACAAGACTGAGTATT 601

Qy 772 ACTAATGAAACATTTAGAAAAACGCAATTATATCCATAA 810
| |||||
Db 602 ACTAATGAAACATTTAGAAAAACGCAATTATATCCATAA 640

RESULT 14

BI596662

LOCUS BI596662 908 bp mRNA linear EST 07-SEP-2001
DEFINITION 603243232F1 NIH_MGC_96 Homo sapiens cDNA clone IMAGE:5285982 5',

mRNA sequence.
 ACCESSION BI596662
 VERSION BI596662.1 GI:15489601
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 908)
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
 cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
 Toshiyuki and Piero Carninci (RIKEN)
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLAM11722 row: o column: 07
 High quality sequence stop: 755.
 FEATURES Location/Qualifiers
 source 1. .908
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5285982"
 /tissue_type="hypothalamus"
 /lab_host="DH10B"
 /clone_lib="NIH_MGC_96"
 /note="Organ: brain; Vector: pBluescriptR (modified
 pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI
 (gtgcag); Oligo-dT primed using primer
 5'-TTTTTTTTTTTTTVN-3', size-selected for average
 insert size 2.3 kb and normalized to ROT 5. This is a
 primary library enriched for full-length clones and
 constructed using the Cap-trapper method (Carninci, in
 preparation). Library constructed by M. Brownstein
 (NIMH/NHGRI, National Institutes of Health). Note: this is
 a NIH_MGC Library."

ORIGIN

Query Match	74.6%	Score	604.4	DB	12	Length	908		
Best Local Similarity	98.6%	Pred. No.	5.3e-156						
Matches	631	Conservative	0	Mismatches	6	Indels	3	Gaps	2

Qy	172	GTGTCGGTCTCCAAGATGGCGGCCGCCCTGGCCGTCTGGTCCGTCTGCTCCGGAGGCCGTG	231
Db	4	GGGTCGGTCTCCAAGATGGCGGCCGCCCTGGCCGTCTGGTCCGTCTGCTCCGGAGGCCGTG	63
Qy	232	ACGGCCAGACTCGTTGGTGTCCCTGTGGTCGTCTCAGTCAGTCACTACAGGACCCCTGGGGGGCT	291
Db	64	ACGGCCAGACTCGTTGGTGTCCCTGTGGTCGTCTCAGTCAGTCACTACAGGACCCCTGGGGGGCT	123

Qy	292	GTTGCCACCTCCGCCGGGGCGAGGAGTCGCTTAAGTGCAGGACCTAAAGTGGACAA	351
Db	124	GTTGCCACCTCCGCCGGGGCGAGGAGTCGCTTAAGTGCAGGACCTAAAGTGGACAA	183
Qy	352	TATATTGTAAAGATCCAAAATAATGACGCTACGCAAGAACCACTAAGTACAAAC	411
Db	184	TATATTGTAAAGATCCAAAATAATGACGCTACGCAAGAACCACTAAGTACAAAC	243
Qy	412	TACACAGCTCATGTTCTGTTCCAGCACCCAACATAACTT-GTAAGGATTCCAGTGG	470
Db	244	TACACAGCTCATGTTCTGTTCCAGCACCCAACATAACTTGGTAAGGATTCCAGTGG	303
Qy	471	CAATGAAACACATTTACTGGGAACGAAGTTGGTTTTCAAGCCATATCTGCCGAAA	530
Db	304	CAATGAAACACATTTACTGGGAACGAAGTTGGTTTTCAAGCCATATCTGCCGAAA	363
Qy	531	TGTAAATGGCTATTCCCTACAAAGTGGCAGTCGCATTGTCTCTTTCTGGATGGTGGG	590
Db	364	TGTAAATGGCTATTCCCTACAAAGTGGCAGTCGCATTGTCTCTTTCTGGATGGTGGG	423
Qy	591	AGCAGATCGATTTACCTGGATACCCCTGCTTGGTTGTTAAAGTTTGCACTGTAGG	650
Db	424	AGCAGATCGATTTACCTGGATACCCCTGCTTGGTTGTTAAAGTTTGCACTGTAGG	483
Qy	651	GTTTGTGAAATTGGGAGCCTAATTGATTTCATTCTTATTCAATGCAGATTGGACC	710
Db	484	GTTT--GTGGAATGGGAGCCTAATTGATTTCATTCTTATTCAATGCAGATTGGACC	541
Qy	711	TTCAGATGGAAGTAGTTACATTATAGATTACTATGAAACCAGACTTACAAGACTGAGTAT	770
Db	542	TTCAGATGGAAGTAGTTACATTATAGATTACTATGAAACCAGACTTACAAGACTGAGTAT	601
Qy	771	TACTAATGAAACATTAGAAAAACGCAATTATATCCATAA	810
Db	602	TACTAATGAAACATTAGAAAAACGCAATTATATCCATAA	641

RESULT 15

AI923178

LOCUS AI923178 599 bp mRNA linear EST 02-SEP-1999
 DEFINITION wn67b10.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2450491 3'
 similar to WP:C02F5.3 CE00039 GTP-BINDING PROTEIN ;, mRNA sequence.
 ACCESSION AI923178
 VERSION AI923178.1 GI:5659142
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 599)
 AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.
 cDNA Library Preparation: M. Bento Soares, Ph.D.
 cDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
 Seq primer: -40UP from Gibco
 High quality sequence stop: 457.

FEATURES Location/Qualifiers
 source 1. .599
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:2450491"
 /tissue_type="squamous cell carcinoma, poorly
 differentiated (4 pooled tumors, including primary and
 metastatic)"
 /dev_stage="adult"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NCI_CGAP_Lu19"
 /note="Organ: lung; Vector: pT7T3D-Pac (Pharmacia) with a
 modified polylinker; 1st strand cDNA was prepared from
 pooled lung tumor tissue, and was then primed with a Not I
 - oligo(dT) primer. Double-stranded cDNA was ligated to
 Eco RI adaptors (Pharmacia), digested with Not I and
 cloned into the Not I and Eco RI sites of the modified
 pT7T3 vector. Library went through one round of
 normalization. Library constructed by Bento Soares and M.
 Fatima Bonaldo. "

ORIGIN

Query Match	73.5%; Score 595.4; DB 9; Length 599;
Best Local Similarity	99.5%; Pred. No. 1.4e-153;
Matches	596; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy	190 GC GG CG CG CT GG CC GT CT GG GT CC GT CT GCT CC GG AG GG CG GT GAC GG CC AG ACT CG TT GG T 249
Db	1 GC GG CG CG CT GG CC GT CT GG GT CC GT CT GCT CC GG AG GG CG GT GAC GG CC AG ACT CG TT GG T 60
Qy	250 GTC CT GT GG TT CG T C T CAG T CACT A CAG GAC CCT GGG GGG CT GT T GCC AC CT CC GG CG GGG 309
Db	61 GTC CT GT GG TT CG T C T CAG T CACT A CAG GAC CCT GGG GGG CT GT T GCC AC CT CC GG CG GGG 120
Qy	310 GGC GAG GAG TCG CTT AAG T GCG AGG ACCT CAA AGT GGG ACA AT AT ATT GT AAG ATCCA 369
Db	121 GGC GAG GAG TCG CTT AAG T GCG AGG ACCT CAA AGT GGG ACA AT AT ATT GT AAG ATCCA 180
Qy	370 AAA ATA AA AT GAC GCT ACG CA AGA ACC AGT TA ACT GT A CAA ACT AC A CAG CT CAT GT TT CC 429
Db	181 AAA ATA AA AT GAC GCT ACG CA AGA ACC AGT TA ACT GT A CAA ACT AC A CAG CT CAT GT TT CC 240
Qy	430 TGT TTT CCAG CAC CC AAC ATA ACT TGT AAG GATT CCAG TGG CAAT GAA ACAC AT TT ACT 489
Db	241 TGT TTT CCAG CAC CC AAC ATA ACT TGT AAG GATT CCAG TGG CAAT GAA ACAC AT TT ACT 300
Qy	490 GGG AAC GAAG TT GG TTT CAAG CCC AT AT CTT GCC GAA AT GT AAT GG CT ATT CCT AC 549

Db |||||||||||||||||||||||||||||||||||||||||||||||
301 GGGAACGAAGTGGTTTTCAAGCCCATATCTTGCCGAAATGTAAATGGCTATTCCCTAC 360

Qy 550 AAAGTGGCAGTCGCATTGTCTCTTTCTTGGATGGTGGGAGCAGATCGATTACCTT 609
 |||||||||||||||||||||||||||||||||||||||||||||||||||
Db 361 AAAGTGGCAGTCGCATTGTCTCTTTCTTGGATGGTGGGAGCAGATCGATTACCTT 420

Qy 610 GGATACCTGCTTGGTTGTTAAAGTTGCACTGTAGGGTTTGTGGAATTGGGAGC 669
 |||||||||||||||||||||||||||||||||||||||||||||||
Db 421 GGATACCTGCTTGGTTGTTAAAGTTGCACTGTANGTTGTGGAATTGGGAGC 480

Qy 670 CTAATTGATTCATTCTATTCAATGCAGATTGTTGGACCTCAGATGGAAGTAGTTAC 729
 |||||||||||||||||||||||||||||||||||||||||||||||
Db 481 CTAATTGATTCATTCTATTCAATGCAGATTGTTGGACCTCAGATGGAAGTAGTTAC 540

Qy 730 ATTATAGATTACTATGGAACCAGACTTACAAGACTGAGTATTACTAATGAAACATTTAG 788
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Db 541 ATTATAGATTACTATGGAACCAGACTTACAAGACTGAGTATTACTAATGAAACATNTAG 599

Search completed: March 4, 2004, 09:16:38

Job time : 2551 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 4, 2004, 05:35:01 ; Search time 3285 Seconds
(without alignments)
10687.323 Million cell updates/sec

Title: US-09-852-100B-1

Perfect score: 810

Sequence: 1 atgcatatttaaaagggtc.....aaacgcaattatatccataa 810

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:
1: gb_ba:
2: gb_htg:
3: gb_in:
4: gb_om:
5: gb_ov:
6: gb_pat:
7: gb_ph:
8: gb_pl:
9: gb_pr:
10: gb_ro:
11: gb_sts:
12: gb_sy:
13: gb_un:
14: gb_vi:
15: em_ba:
16: em_fun:
17: em_hum:
18: em_in:
19: em_mu:
20: em_om:
21: em_or:
22: em_ov:
23: em_pat:
24: em_ph:
25: em_pl:
26: em_ro:
27: em_sts:

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28: em_un:*
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35: em_htg_rod:*
36: em_htg_mam:*
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39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Result No.	Score	Query				Description
		Match	Length	DB	ID	
1	810	100.0	810	6	BD243134	BD243134 6-Protein
2	810	100.0	1246	9	AF353990	AF353990 Homo sapi
3	645	79.6	984	9	BC029486	BC029486 Homo sapi
4	602.8	74.4	970	6	BD139411	BD139411 Extended
5	499	61.6	508	6	BD265227	BD265227 Compounds
6	499	61.6	508	6	BD265239	BD265239 Compounds
7	499	61.6	508	6	AR401213	AR401213 Sequence
8	499	61.6	508	6	AR401225	AR401225 Sequence
9	499	61.6	508	6	AX192666	AX192666 Sequence
10	499	61.6	508	6	AX192678	AX192678 Sequence
11	471.6	58.2	630	10	AF353993	AF353993 Mus muscu
12	436.8	53.9	440	6	BD076181	BD076181 5' EST of
c 13	430.6	53.2	193660	2	AC102262	AC102262 Mus muscu
14	425.2	52.5	455	6	BD076249	BD076249 5' EST of
15	411.4	50.8	487	6	AX892343	AX892343 Sequence
16	411.4	50.8	487	6	BD027876	BD027876 Sequence
c 17	354	43.7	183425	9	AC097064	AC097064 Homo sapi
c 18	354	43.7	239704	9	AC099791	AC099791 Homo sapi
c 19	325.4	40.2	228458	2	AC097670	AC097670 Rattus no
20	299	36.9	176056	10	AC073437	AC073437 Mus muscu
21	299	36.9	196421	10	AL672100	AL672100 Mouse DNA
22	276	34.1	185576	2	AC025691	AC025691 Homo sapi
c 23	250.4	30.9	231150	2	AC114195	AC114195 Rattus no
24	244.4	30.2	157999	2	AC117088	AC117088 Rattus no
25	209.8	25.9	277191	2	AC109077	AC109077 Rattus no
26	186.2	23.0	167627	9	AC079382	AC079382 Homo sapi
27	145.6	18.0	178068	2	AC142046	AC142046 Rattus no
c 28	114	14.1	129705	2	AC133258	AC133258 Rattus no
29	114	14.1	239113	2	AC094034	AC094034 Rattus no
30	114	14.1	324462	2	AC137263	AC137263 Rattus no
c 31	107.6	13.3	145871	2	AC143611	AC143611 Macaca mu
32	99.8	12.3	298	6	E25986	E25986 Blastocyst
33	99.2	12.2	240950	2	AC098287	AC098287 Rattus no

c	34	97.8	12.1	131215	10	AL671140	AL671140 Mouse DNA
c	35	73.2	9.0	198395	2	AC101700	AC101700 Mus muscu
	36	64.6	8.0	128444	2	AC019924	AC019924 Drosophil
	37	64.6	8.0	132637	2	AC006092	AC006092 Drosophil
c	38	64.6	8.0	149592	2	AC005718	AC005718 Drosophil
c	39	64.6	8.0	179139	3	AC099307	AC099307 Drosophil
c	40	64.6	8.0	188633	3	AC007175	AC007175 Drosophil
c	41	64.6	8.0	305150	3	AE003453	AE003453 Drosophil
	42	64.4	8.0	1052	3	AY061343	AY061343 Drosophil
	43	58.2	7.2	155623	5	AL929239	AL929239 Zebrafish
	44	58.2	7.2	239459	2	BX322568	BX322568 Danio rer
c	45	54.6	6.7	214455	2	AC118451	AC118451 Rattus no

ALIGNMENTS

RESULT 1

BD243134

LOCUS BD243134 810 bp DNA linear PAT 17-JUL-2003
 DEFINITION 6-Protein-bound receptor-like protein, polynucleotide encoded by it, and method of use thereof.
 ACCESSION BD243134
 VERSION BD243134.1 GI:33052904
 KEYWORDS JP 2002527064-A/1.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 810)
 AUTHORS Ozenberger, B.A., Kajkowski, E.M. and Lo, C.H.F.
 TITLE 6-Protein-bound receptor-like protein, polynucleotide encoded by it, and method of use thereof
 JOURNAL Patent: JP 2002527064-A 1 27-AUG-2002;
 AMERICAN HOME PRODUCTS CORP
 COMMENT OS Homo sapiens (human)
 PN JP 2002527064-A/1
 PD 27-AUG-2002
 PF 13-OCT-1999 JP 2000576015
 PR 13-OCT-1998 US 60/104104
 PI BRADLEY ALTON OZENBERGER, EILEEN MARIE KAJKOWSKI, CHING HSIUNG
 PI FREDERICK LO
 PC C12N15/09, A61K45/00, A61P43/00, C07K14/705, C12N1/15, C12N1/19, PC
 C12N1/21,
 PC C12N5/10, C12Q1/02, C12Q1/68, G01N33/15, G01N33/50, G01N33/53, PC
 G01N33/566,
 PC C12N15/00, C12N5/00
 CC 6-Protein-bound receptor-like protein, polynucleotide encoded
 CC by it, and
 CC method of use thereof
 FH Key Location/Qualifiers
 FT source 1..810
 FT /organism='Homo sapiens (human)'.
 FEATURES Location/Qualifiers
 source 1..810
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 /mol_type="genomic DNA"

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ORIGIN

Query Match 100.0%; Score 810; DB 6; Length 810;
Best Local Similarity 100.0%; Pred. No. 2.2e-206;
Matches 810; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGCATATTAAAAGGGTCTCCAATGTGATTCCACGGGCTCACGGGCAGAAGAACACG 60
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Qy 61 CGAAGAGACGGAACTGGCCTCTATCCTATGCGAGGTCCCTTAAGAACCTGCCCTGTTG 120
Db |||||||
Qy 61 CGAAGAGACGGAACTGGCCTCTATCCTATGCGAGGTCCCTTAAGAACCTGCCCTGTTG 120
Db |||||||
Qy 121 CCCTTCTCCCTCCGCTCCTGGCGGAGGCGGAAGCGGAAGTGGCGAGAAAGTGTGGTC 180
Db |||||||
Qy 121 CCCTTCTCCCTCCGCTCCTGGCGGAGGCGGAAGCGGAAGTGGCGAGAAAGTGTGGTC 180
Db |||||||
Qy 181 TCCAAGATGGCGGCCGCTGGCGTCTGGTCCGTCTGCTCCGGAGGCCGTGACGGCCAGA 240
Db |||||||
Qy 181 TCCAAGATGGCGGCCGCTGGCGTCTGGTCCGTCTGCTCCGGAGGCCGTGACGGCCAGA 240
Db |||||||
Qy 241 CTCGTTGGTGTCCGTGGTCGTCAGTCACTACAGGACCTGGGGGCTGTTGCCACC 300
Db |||||||
Qy 241 CTCGTTGGTGTCCGTGGTCGTCAGTCACTACAGGACCTGGGGGCTGTTGCCACC 300
Db |||||||
Qy 301 TCCGCCGGGGCGAGGAGTCGCTTAAGTGCAGGACCTCAAAGTGGACAATATATTGT 360
Db |||||||
Qy 301 TCCGCCGGGGCGAGGAGTCGCTTAAGTGCAGGACCTCAAAGTGGACAATATATTGT 360
Db |||||||
Qy 361 AAAGATCCAAAATAATGACGCTACGCAAGAACCAAGTTAACTGTACAAACTACACAGCT 420
Db |||||||
Qy 361 AAAGATCCAAAATAATGACGCTACGCAAGAACCAAGTTAACTGTACAAACTACACAGCT 420
Db |||||||
Qy 421 CATTTCCGTGTTCCAGCACCCACATAACTGTAAGGATTCCAGTGGCAATGAAACA 480
Db |||||||
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Qy 481 CATTAACTGGAACGAAGTTGGTTTTCAAGCCCATACTTGCAAGGGAAATGTAAATGGC 540
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Db 721 AGTAGTTACATTATAGATTACTATGGAACCAGACTTACAAGACTGAGTATTACTAATGAA 780
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Db 781 ACATTTAGAAAAACGCAATTATATCCATAA 810

RESULT 2

AF353990

LOCUS AF353990 1246 bp mRNA linear PRI 29-MAY-2001
DEFINITION Homo sapiens beta-amyloid binding protein precursor (BBP) mRNA, complete cds.
ACCESSION AF353990
VERSION AF353990.1 GI:13625458
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1246)
AUTHORS Kajkowski,E.M., Lo,C.F., Ning,X., Walker,S., Sofia,H.J., Wang,W., Edris,W., Chanda,P., Wagner,E., Vile,S., Ryan,K., McHendry-Rinde,B., Smith,S.C., Wood,A., Rhodes,K.J., Kennedy,J.D., Bard,J., Jacobsen,J.S. and Ozenberger,B.A.
TITLE beta -Amyloid peptide-induced apoptosis regulated by a novel protein containing a g protein activation module
JOURNAL J. Biol. Chem. 276 (22), 18748-18756 (2001)
MEDLINE 21276355
PUBMED 11278849
REFERENCE 2 (bases 1 to 1246)
AUTHORS Ozenberger,B.A., Kajkowski,E., Jacobsen,J.S., Bard,J. and Walker,S.
TITLE Direct Submission
JOURNAL Submitted (27-FEB-2001) Wyeth Neuroscience, CN 8000, Princeton, NJ 08543, USA
FEATURES Location/Qualifiers
source 1. 1246
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/chromosome="1"
gene 1. .1246
/gene="BBP"
CDS 304. .927
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/codon_start=1
/product="beta-amyloid-binding protein precursor"
/protein_id="AAK35064.1"
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ORIGIN

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 Best Local Similarity 100.0%; Pred. No. 2.4e-206;
 Matches 810; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1 ATGCATATTTAAAAGGGTCTCCAATGTGATTCCACGGGCTCACGGGCAGAACACG	60
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Db	178 CGAAGAGACGGAACTGGCCTCATCCTATGCGAGGTCCCTTAAGAACCTGCCCTGTTG	237
Qy	121 CCCTTCTCCCTCCCGCTCCTGGCGGAGGCGGAAGCGGAAGTGGCGAGAAAGTGTGGTC	180
Db	238 CCCTTCTCCCTCCCGCTCCTGGCGGAGGCGGAAGCGGAAGTGGCGAGAAAGTGTGGTC	297
Qy	181 TCCAAGATGGCGGCCGCCTGGCGTCTGGTCCGTCTGCTCCGGAGGCCGTGACGGCCAGA	240
Db	298 TCCAAGATGGCGGCCGCCTGGCGTCTGGTCCGTCTGCTCCGGAGGCCGTGACGGCCAGA	357
Qy	241 CTCGTTGGTGTCCGTGGTTCGTCTCAGTCACTACAGGACCTGGGGCTGTTGCCACC	300
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Qy	301 TCCGCCGGGGCGAGGAGTCGCTTAAGTGCAGGACCTCAAAGTGGACAATATATTGT	360
Db	418 TCCGCCGGGGCGAGGAGTCGCTTAAGTGCAGGACCTCAAAGTGGACAATATATTGT	477
Qy	361 AAAGATCCAAAAATAATGACGCTACGCAAGAACAGTTAAGTACAAACTACACAGCT	420
Db	478 AAAGATCCAAAAATAATGACGCTACGCAAGAACAGTTAAGTACAAACTACACAGCT	537
Qy	421 CATTTTCCTGTTCCAGCACCAACATAACTTGTAAAGGATTCCAGTGGCAATGAAACA	480
Db	538 CATTTTCCTGTTCCAGCACCAACATAACTTGTAAAGGATTCCAGTGGCAATGAAACA	597
Qy	481 CATTTCCTGGAACGAAGTGGTTTTCAAGCCATATCTGCCGAAATGTAAATGGC	540
Db	598 CATTTCCTGGAACGAAGTGGTTTTCAAGCCATATCTGCCGAAATGTAAATGGC	657
Qy	541 TATTCCCTACAAAGTGGCAGTCGATTGTCTTTTCTGGATGGTGGGAGCAGATCGA	600
Db	658 TATTCCCTACAAAGTGGCAGTCGATTGTCTTTTCTGGATGGTGGGAGCAGATCGA	717
Qy	601 TTTTACCTGGATACCCTGCTTGGTTGTTAAAGTTTGCAGTGTAGGGTTTGGA	660
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Qy	661 ATTGGGAGCCTAATTGATTTCATTCTATTCAATGCAGATTGGACCTTCAGATGGA	720
Db	778 ATTGGGAGCCTAATTGATTTCATTCTATTCAATGCAGATTGGACCTTCAGATGGA	837

QY	721 AGTAGTTACATTATAGATTACTATGGAACCAGACTTACAAGACTGAGTATTACTAATGAA	780
Db	838 AGTAGTTACATTATAGATTACTATGGAACCAGACTTACAAGACTGAGTATTACTAATGAA	897
QY	781 ACATTTAGAAAAACGCAATTATATCCATAA	810
Db	898 ACATTTAGAAAAACGCAATTATATCCATAA	927

RESULT 3
BC029486

LOCUS BC029486 984 bp mRNA linear PRI 06-OCT-2003

DEFINITION Homo sapiens beta-amyloid binding protein precursor, mRNA (cDNA clone MGC:32941 IMAGE:5271098), complete cds.

ACCESSION BC029486

VERSION BC029486.1 GI:20809565

KEYWORDS MGC.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 984)

AUTHORS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E., Schnurch, A., Schein, J.E., Jones, S.J. and Marra, M.A.

TITLE Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

MEDLINE 22388257

PUBMED 12477932

REFERENCE 2 (bases 1 to 984)

AUTHORS Strausberg, R.

TITLE Direct Submission

JOURNAL Submitted (01-MAY-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>

COMMENT Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

cDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shiraki
 Toshiyuki and Piero Carninci (RIKEN)
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Sequencing Group at the Stanford Human Genome
 Center, Stanford University School of Medicine, Stanford, CA 94305
 Web site: <http://www-shgc.stanford.edu>
 Contact: (Dickson, Mark) mcd@paxil.stanford.edu
 Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
 R. M.

Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRAK Plate: 48 Row: b Column: 24
 This clone was selected for full length sequencing because it
 passed the following selection criteria: matched mRNA gi: 17738309.

FEATURES	Location/Qualifiers
source	1. .984 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="MGC:32941 IMAGE:5271098" /tissue_type="Testis" /clone_lib="NIH_MGC_97" /lab_host="DH10B" /note="Vector: pBluescript"
gene	1. .984 /gene="BBP" /db_xref="LocusID:83941"
CDS	22. .645 /codon_start=1 /product="beta-amyloid binding protein precursor" /protein_id="AAH29486.1" /db_xref="GI:20809566" /db_xref="LocusID:83941" /translation="MAAAWPSGPSAPEAVTARLVGVLFVSVTTGPWGAVATSAGGEE SLKCEDLKVGQYICKDPKINDATQEPMVNCTNYTAHVSCFPAPNITCKDSSGNETHFTG NEVGGFKPISCRNVNGYSYKVAVALSLFLGWLGLGADRFYLGYPALGLLKFCCTVGFCGIG SLIDFILISMHQIVGPGSDGSSYIIDYYGTRLTRLSITNETFRKTQLYP"
misc_feature	385. .525 /note="XynA; Region: Predicted membrane protein [Function unknown]" /db_xref="CDD:COG2314"

ORIGIN

Query Match	79.6%	Score	645;	DB	9;	Length	984;		
Best Local Similarity	100.0%	Pred. No.	4.8e-162;						
Matches	645;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;

Qy	166	GAGAAAGTGTGGTCTCCAAGATGGCGGCCGCTGGCCGTCTGGTCCGTCTGCTCCGGAG	225
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Db	61	GCCGTGACGGCCAGACTCGTTGGTGTCCCTGTGGTTCGTCTCAGTCACTACAGGACCTGG	120
Qy	286	GGGGCTGTTGCCACCTCCGCCGGGGCGAGGAGTCGCTTAAGTGCAGGACCTCAAAGTG	345

Db	121	GGGGCTGTTGCCACCTCCGCCGGGGCGAGGAGTCGCTTAAGTGCAGGACCTCAAAGTG	180
Qy	346	GGACAATATATTGTAAAGATCCAAAATAAATGACGCTACGCAAGAACCACTTAACGT	405
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Qy	406	ACAAACTACACAGCTCATGTTCCCTGTTTCCAGCACCCAACATAACTTGTAAAGGATTCC	465
Db	241	ACAAACTACACAGCTCATGTTCCCTGTTTCCAGCACCCAACATAACTTGTAAAGGATTCC	300
Qy	466	AGTGGCAATGAAACACATTACTGGGAACGAAGTGGTTTTCAAGCCATATCTGC	525
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Db	361	CGAAATGTAAATGGCTATTCCCTACAAAGTGGCAGTCGCATTGTCTCTTTCTTGGATGG	420
Qy	586	TTGGGAGCAGATCGATTTACCTGGATACCCTGCTTGGTTGTTAAAGTTGCAC	645
Db	421	TTGGGAGCAGATCGATTTACCTGGATACCCTGCTTGGTTGTTAAAGTTGCAC	480
Qy	646	GTAGGGTTTGTGAAATTGGGAGCCTAATTGATTCATTCTTATTCAATGCAGATTGTT	705
Db	481	GTAGGGTTTGTGAAATTGGGAGCCTAATTGATTCATTCTTATTCAATGCAGATTGTT	540
Qy	706	GGACCTTCAGATGGAAGTAGTTACATTATAGATTACTATGGAACCAGACTTACAAGACTG	765
Db	541	GGACCTTCAGATGGAAGTAGTTACATTATAGATTACTATGGAACCAGACTTACAAGACTG	600
Qy	766	AGTATTACTAATGAAACATTAGAAAAACGCAATTATATCCATAA	810
Db	601	AGTATTACTAATGAAACATTAGAAAAACGCAATTATATCCATAA	645

RESULT 4

BD13941:

LOCUS BD139411 970 bp DNA linear PAT 18-SEP-2002
DEFINITION Extended cDNA of secretory protein.
ACCESSION BD139411
VERSION BD139411.1 GI:23234356
KEYWORDS JP 2002508182-A/163.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 970)
AUTHORS Bougueret,L., Duclert,A. and Edwards,J.B.D.M.
TITLE Extended cDNA of secretory protein
JOURNAL Patent: JP 2002508182-A 163 19-MAR-2002;
GENSET
COMMENT OS Homo sapiens (human)
PN JP 2002508182-A/163
PD 19-MAR-2002
PF 17-DEC-1998 JP 2000539136
PR 17-DEC-1997 US 60/069957, 09-FEB-1998 US 60/074121 PR

13-APR-1998 US 60/081563,10-AUG-1998 US 60/096116 PI LYDIE
 BOUGUELERET,AYMERIC DUCLERT,JEAN BAPTISTE DUMAS MILNE PI EDWARDS
 PC C12N15/09,C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19, PC
 C12N1/21,
 PC C12N5/10,C12P21/02,C12Q1/68,C12N15/00,C12N5/00,C12N15/00 CC
 Von Heijne matrix
 CC score 5.5
 CC seq LVGVLFVSVTTG/PW
 FH Key Location/Qualifiers
 FT CDS 12. .497
 FT sig_peptide 12. .104
 FT polyA_signal 935. .940
 FT polyA_site 955. .967.
FEATURES
 source Location/Qualifiers
 1. .970
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
ORIGIN
 Query Match 74.4%; Score 602.8; DB 6; Length 970;
 Best Local Similarity 98.4%; Pred. No. 1e-150;
 Matches 624; Conservative 5; Mismatches 3; Indels 2; Gaps 2;

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 Db 2 GGTCTCCAAGATGGCGGCCCTGGCGTCTGGTCCGKCTGCTCCGGAGGCCGTGACGGC 61

 Qy 237 CAGACTCGTTGGTGTCTGTGGTCGTCACTACAGGACCTGGGGGCTGTTGC 296
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 Db 62 CAGACTCGTTGGTGTCTGTGGTCGTCACTACAGGACCTGGGGGCTGTTGC 121

 Qy 297 CACCTCCGCCGGGGCGAGGAGTCGCTTAAGTGCAGGACCTCAAAGTGGACAATATAT 356
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 Db 122 CACCTCCGCCGGGGCGAGGAGTCGCTTAAGTGCAGGACCTCAAAGTGGACAATATAT 181

 Qy 357 TTGTAAAGATCCAAAATAATGACGCTACGCAAGAACCTAGTTAAGTACAAACTACAC 416
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 Db 182 TTGTAAAGATCCAAAATAATGACGCTACGCAAGAACCTAGTTAAGTACAAACTACAC 241

 Qy 417 AGCTCATTTCTGTTCCAGCACCCAAACATAACTTGTAAAGGATTCCAGTGGCAATGA 476
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 Db 242 AGCTCATTTCTGTTCCAGCACCCAAACATAACTTGTAAAGGATTCCAGTGGCAATGA 301

 Qy 477 AACACATTTACTGGAACGAAGTTGGTTTTCAAGCCCATACTTGGCAATGTAAA 536
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 Db 302 AACACATTTACTGGAACGAAGTTGGTTTTCAAGCCCATACTTGGCAATGTAAA 361

 Qy 537 TGGCTATTCTACAAAGTGGCAGTCGATTGTCTCTTCTGGATGGTGGAGCAGA 596
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 Db 362 TGGCTATTCTACAAATG-AGCAGTCGCA-TGTCTCTTCTGGATGGTGGAGCAGA 419

 Qy 597 TCGATTTACCTGGATACCCTGCTTGGTTGTTAAAGTTGCAGTGTAGGGTTTG 656
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 Db 420 TCGATTTACCTGGATACCCTGCTTGGTTGTTAAABTTTYGCAGTGTAGGGTTKG 479

 Qy 657 TGGAAATTGGGAGCCTAATTGATTCTATTCAATGCAGATTGGACCTTCAGA 716

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Qy      717 TGGAAGTAGTTACATTATAGATTACTATGGAACCAGACTTACAAGACTGAGTATTACTAA 776
Db      |||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|
540 TGGAAGTAGTTACATTATAGATTACTATGGAACCAGACTTACAAGACTGAGTATTACTAA 599

Qy      777 TGAAACATTAGAAAAACGCAATTATATCCATAA 810
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600 TGAAACATTAGAAAAACGCAATTATATCCATAA 633

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RESULT 5

BD265227

LOCUS BD265227 508 bp DNA linear PAT 17-JUL-2003
 DEFINITION Compounds for immunotherapy and diagnosis of colonic cancer and method of using the same.
 ACCESSION BD265227
 VERSION BD265227.1 GI:33074995
 KEYWORDS JP 2002533082-A/225.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 508)
 AUTHORS Xu,J., Lodes,M.J., Secrist,H., Benson,D.R., Meagher,M.J., Stolk,J.,
 Wang,T. and Yuqiu,J.
 TITLE Compounds for immunotherapy and diagnosis of colonic cancer and method of using the same
 JOURNAL Patent: JP 2002533082-A 225 08-OCT-2002;
 CORIXA CORP
 COMMENT OS Homo sapiens (human)
 PN JP 2002533082-A/225
 PD 08-OCT-2002
 PF 23-DEC-1999 JP 2000589697
 PR 23-DEC-1998 US 09/221298,02-JUL-1999 US 09/347496 PR
 22-SEP-1999 US 09/401064,19-NOV-1999 US 09/444242 PR
 02-DEC-1999 US 09/454150
 PI JIANGCHUN XU, MICHAEL J LODES, HEATHER SECRIEST, DARIN R BENSON,
 PI MADELEINE JOY MEAGHER, JOHN STOLK, TONGTONG WANG, JIANG YUQIU PC
 C12N15/09, A61K31/711, A61K35/14, A61K38/00, A61K39/00, A61K39/395, PC
 A61K39/395,
 PC A61P35/00, C07K14/47, C07K16/18, C07K19/00, C12N1/15, C12N1/19, PC
 C12N1/21,
 PC
 C12N5/06, C12N5/10, C12Q1/02, C12Q1/68, G01N33/53, G01N33/53, G01N33/ PC
 566,
 PC G01N33/574, G01N33/577, G01N33/58, C12N15/00, C12N5/00, C12N5/00,
 PC A61K37/02
 CC Compounds for immunotherapy and diagnosis of colonic cancer
 CC and method of
 CC using the same
 FH Key Location/Qualifiers
 FT source 1. .508
 FT /organism='Homo sapiens (human)'.
 FEATURES Location/Qualifiers
 source 1. .508

/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 61.6%; Score 499; DB 6; Length 508;
Best Local Similarity 100.0%; Pred. No. 6.9e-123;
Matches 499; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	312 CGAGGAGTCGCTTAAGTGCAGGGACCTCAAAGTGGACAATATATTGTAAAGATCCAAA	371
Db	1 CGAGGAGTCGCTTAAGTGCAGGGACCTCAAAGTGGACAATATATTGTAAAGATCCAAA	60
Qy	372 AATAAATGACGCTACGCAAGAACAGTTAACGTACAAACTACACAGCTCATGTTCTG	431
Db	61 AATAAATGACGCTACGCAAGAACAGTTAACGTACAAACTACACAGCTCATGTTCTG	120
Qy	432 TTTTCCAGCACCCAACATAACTTGTAAAGGATTCCAGTGGCAATGAAACACATTACTGG	491
Db	121 TTTTCCAGCACCCAACATAACTTGTAAAGGATTCCAGTGGCAATGAAACACATTACTGG	180
Qy	492 GAACGAAGTTGGTTTTCAAGCCCATACTTGTAAAGGATTCCAGTGGCAATGAAACACATTACTGG	551
Db	181 GAACGAAGTTGGTTTTCAAGCCCATACTTGTAAAGGATTCCAGTGGCAATGAAACACATTACTGG	240
Qy	552 AGTGGCAGTCGCATTGTCTCTTTCTGGATGGTGGAGCAGATCGATTACCTTGG	611
Db	241 AGTGGCAGTCGCATTGTCTCTTTCTGGATGGTGGAGCAGATCGATTACCTTGG	300
Qy	612 ATACCCTGCTTGGTTGTAAAGTTGCACGTAGGGTTTGGAATTGGAGCCT	671
Db	301 ATACCCTGCTTGGTTGTAAAGTTGCACGTAGGGTTTGGAATTGGAGCCT	360
Qy	672 AATTGATTTCATTCTATTCAATGCAGATTGGACCTTCAGATGGAAGTAGTTACAT	731
Db	361 AATTGATTTCATTCTATTCAATGCAGATTGGACCTTCAGATGGAAGTAGTTACAT	420
Qy	732 TATAGATTACTATGGAACCAGACTTACAAGACTGAGTATTACTAATGAAACATTAGAAA	791
Db	421 TATAGATTACTATGGAACCAGACTTACAAGACTGAGTATTACTAATGAAACATTAGAAA	480
Qy	792 AACGCAATTATATCCATAA	810
Db	481 AACGCAATTATATCCATAA	499

RESULT 6

BD265239

LOCUS BD265239 508 bp DNA linear PAT 17-JUL-2003
DEFINITION Compounds for immunotherapy and diagnosis of colonic cancer and method of using the same.
ACCESSION BD265239
VERSION BD265239.1 GI:33075007
KEYWORDS JP 2002533082-A/237.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 AUTHORS 1 (bases 1 to 508)
 Xu,J., Lodes,M.J., Secrist,H., Benson,D.R., Meagher,M.J., Stolk,J.,
 Wang,T. and Yuqiu,J.
 TITLE Compounds for immunotherapy and diagnosis of colonic cancer and
 method of using the same
 JOURNAL Patent: JP 2002533082-A 237 08-OCT-2002;
 CORIXA CORP
 COMMENT OS Homo sapiens (human)
 PN JP 2002533082-A/237
 PD 08-OCT-2002
 PF 23-DEC-1999 JP 2000589697
 PR 23-DEC-1998 US 09/221298,02-JUL-1999 US 09/347496 PR
 22-SEP-1999 US 09/401064,19-NOV-1999 US 09/444242 PR
 02-DEC-1999 US 09/454150
 PI JIANGCHUN XU, MICHAEL J LODES, HEATHER SECRIEST, DARIN R BENSON,
 PI MADELEINE JOY MEAGHER, JOHN STOLK, TONGTONG WANG, JIANG YUQIU PC
 C12N15/09, A61K31/711, A61K35/14, A61K38/00, A61K39/00, A61K39/395, PC
 A61K39/395,
 PC A61P35/00, C07K14/47, C07K16/18, C07K19/00, C12N1/15, C12N1/19, PC
 C12N1/21,
 PC
 C12N5/06, C12N5/10, C12Q1/02, C12Q1/68, G01N33/53, G01N33/53, G01N33/ PC
 566,
 PC G01N33/574, G01N33/577, G01N33/58, C12N15/00, C12N5/00, C12N5/00,
 PC A61K37/02
 CC Compounds for immunotherapy and diagnosis of colonic cancer
 CC and method of
 CC using the same
 FH Key Location/Qualifiers
 FT source 1..508
 FT /organism='Homo sapiens (human)'.
 FEATURES Location/Qualifiers
 source 1..508
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db xref="taxon:9606"

ORIGIN

Query Match 61.6%; Score 499; DB 6; Length 508;
Best Local Similarity 100.0%; Pred. No. 6.9e-123;
Matches 499; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      312 CGAGGGAGTCGCTTAAGTGCAGGGACCTCAAAGTGGGACAATATATTGTAAAGATCCAA 371
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Db      1 CGAGGGAGTCGCTTAAGTGCAGGGACCTCAAAGTGGGACAATATATTGTAAAGATCCAA 60

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Qy 372 AATAAAATGACGCTACGCAAGAACCGAGTTAAGTGTACAAAACACAGCTCATGTTCCCTG 431
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QY 432 TTTTCCAGCACCAACATAACTTGTAAGGATTCCAGTGGCAATGAAACACATTACTGG 491

Db 121 TTTTCCAGCACCCAACATAACTTGTAAGGATTCCAGTGGCAATGAAACACATTTACTGG 180

Db 181 GAACGAAGTTGGTTTTCAAGCCCATATCTGCCGAAATGTAAATGGCTATTCTACAA 240
 Qy 552 AGTGGCAGTCGCATTGTCTCTTTCTTGGATGGTGGAGCAGATCGATTTACCTTGG 611
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 Db 241 AGTGGCAGTCGCATTGTCTCTTTCTTGGATGGTGGAGCAGATCGATTTACCTTGG 300
 Qy 612 ATACCCTGCTTGTTGGTTGTTAAAGTTTGCACGTAGGGTTTGTGAAATTGGGAGCCT 671
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 Db 301 ATACCCTGCTTGTTGGTTGTTAAAGTTTGCACGTAGGGTTTGTGAAATTGGGAGCCT 360
 Qy 672 AATTGATTCATTCTTATTCAATGCAGATTGGACCTCAGATGGAAGTAGTTACAT 731
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 Qy 732 TATAGATTACTATGGAACCAGACTTACAAGACTGAGTATTACTAATGAAACATTAGAAA 791
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 Db 421 TATAGATTACTATGGAACCAGACTTACAAGACTGAGTATTACTAATGAAACATTAGAAA 480
 Qy 792 AACGCAATTATATCCATAA 810
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 Db 481 AACGCAATTATATCCATAA 499

RESULT 7

AR401213

LOCUS AR401213 508 bp DNA linear PAT 18-DEC-2003
 DEFINITION Sequence 233 from patent US 6623923.
 ACCESSION AR401213
 VERSION AR401213.1 GI:40148513
 KEYWORDS .
 SOURCE Unknown.
 ORGANISM Unknown.
 Unclassified.
 REFERENCE 1 (bases 1 to 508)
 AUTHORS Xu,J., Lodes,M.J., Secrist,H., Meagher,M.J., Stolk,J., Benson,D.R.
 and Wang,T.
 TITLE Compounds for immunotherapy and diagnosis of colon cancer and
 methods for their use
 JOURNAL Patent: US 6623923-A 233 23-SEP-2003;
 FEATURES Location/Qualifiers
 source 1. .508
 /organism="unknown"
 /mol_type="genomic DNA"

ORIGIN

Query Match 61.6%; Score 499; DB 6; Length 508;
 Best Local Similarity 100.0%; Pred. No. 6.9e-123;
 Matches 499; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 312 CGAGGAGTCGCTTAAGTGCAGGGACCTCAAAGTGGACAATATTTGTAAAGATCCAAA 371
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 Db 61 AATAAATGACGCTACGCAAGAACCAAGTTAACTGTACAAACTACACAGCTCATGTTCTG 120

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 Db 181 GAACGAAGTTGGTTTTCAAGCCCATACTTGCGAAATGTAAATGGCTATTCTACAA 240
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 Qy 552 AGTGGCAGTCGCATTGTCTCTTTCTGGATGGTGGAGCAGATCGATTTACCTGG 611
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 Qy 792 AACGCAATTATATCCATAA 810
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 Db 481 AACGCAATTATATCCATAA 499

RESULT 8

AR401225

LOCUS	AR401225	508 bp	DNA	linear	PAT 18-DEC-2003
DEFINITION	Sequence 245 from patent US 6623923.				
ACCESSION	AR401225				
VERSION	AR401225.1 GI:40148525				
KEYWORDS	.				
SOURCE	Unknown.				
ORGANISM	Unknown. Unclassified.				
REFERENCE	1 (bases 1 to 508)				
AUTHORS	Xu, J., Lodes, M.J., Secrist, H., Meagher, M.J., Stolk, J., Benson, D.R. and Wang, T.				
TITLE	Compounds for immunotherapy and diagnosis of colon cancer and methods for their use				
JOURNAL	Patent: US 6623923-A 245 23-SEP-2003;				
FEATURES	Location/Qualifiers				
source	1..508 /organism="unknown" /mol_type="genomic DNA"				

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Query Match 61.6%; Score 499; DB 6; Length 508;
 Best Local Similarity 100.0%; Pred. No. 6.9e-123;
 Matches 499; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 181 GAACGAAGTTGGTTTTCAAGCCCATACTGCCGAAATGTAAATGGCTATTCTACAA 240
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 Qy 612 ATACCCTGCTTGGGTTGTTAAAGTTTGCAGTGTAGGGTTTGTGGAATTGGGAGCCT 671
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 Db 301 ATACCCTGCTTGGGTTGTTAAAGTTTGCAGTGTAGGGTTTGTGGAATTGGGAGCCT 360
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 Db 361 AATTGATTCATTCTATTCAATGCAGATTGGACCTTCAGATGGAAGTAGTTACAT 420
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 Db 421 TATAGATTACTATGGAACCAGACTTACAAGACTGAGTATTACTAATGAAACATTAGAAA 480
 Qy 792 AACGCAATTATATCCATAA 810
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 Db 481 AACGCAATTATATCCATAA 499

RESULT 9

AX192666

LOCUS AX192666 508 bp DNA linear PAT 15-AUG-2001
 DEFINITION Sequence 233 from Patent WO0149716.
 ACCESSION AX192666
 VERSION AX192666.1 GI:15210622
 KEYWORDS .
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1
 AUTHORS Xu, J., Lodes, M.J., Secrist, H., Benson, D.R., Meagher, M.J.,
 Stolk, J.A., King, G.E., Wang, T. and Jiang, Y.
 TITLE Compounds for immunotherapy and diagnosis of colon cancer and
 methods for their use
 JOURNAL Patent: WO 0149716-A 233 12-JUL-2001;
 CORIXA CORPORATION (US)
 FEATURES Location/Qualifiers
 source 1..508
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 /mol_type="unassigned DNA"

/db_xref="taxon:9606"

ORIGIN

Query Match 61.6%; Score 499; DB 6; Length 508;
Best Local Similarity 100.0%; Pred. No. 6.9e-123;
Matches 499; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 312 CGAGGAGTCGCTTAAGTGCAGGACCTCAAAGTGGACAATATATTGTAAAGATCCAAA 371
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Qy 432 TTTCCAGCACCCAACATAACTGTAAGGATTCCAGTGGCAATGAAACACATTACTGG 491
Db 121 TTTCCAGCACCCAACATAACTGTAAGGATTCCAGTGGCAATGAAACACATTACTGG 180

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Db 181 GAACGAAGTTGGTTTTCAAGCCCATATCTGCCGAAATGTAAATGGCTATTCTACAA 240

Qy 552 AGTGGCAGTCGATTGTCCTTTCTGGATGGTGGAGCAGATCGATTTACCTTGG 611
Db 241 AGTGGCAGTCGATTGTCCTTTCTGGATGGTGGAGCAGATCGATTTACCTTGG 300

Qy 612 ATACCCTGCTTGGTTGTTAAAGTTGCAGTGAGGTTTGGAATTGGAGCCT 671
Db 301 ATACCCTGCTTGGTTGTTAAAGTTGCAGTGAGGTTTGGAATTGGAGCCT 360

Qy 672 AATTGATTCATTCTATTCAATGCAGATTGGACCTTCAGATGGAAGTAGTTACAT 731
Db 361 AATTGATTCATTCTATTCAATGCAGATTGGACCTTCAGATGGAAGTAGTTACAT 420

Qy 732 TATAGATTACTATGGAACCAGACTTACAAGACTGAGTATTACTAATGAAACATTAGAAA 791
Db 421 TATAGATTACTATGGAACCAGACTTACAAGACTGAGTATTACTAATGAAACATTAGAAA 480

Qy 792 AACGCAATTATATCCATAA 810
Db 481 AACGCAATTATATCCATAA 499

RESULT 10

AX192678

LOCUS AX192678 508 bp DNA linear PAT 15-AUG-2001

DEFINITION Sequence 245 from Patent WO0149716.

ACCESSION AX192678

VERSION AX192678.1 GI:15210634

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Xu, J., Lodes, M.J., Secrist, H., Benson, D.R., Meagher, M.J.,

Stolk, J.A., King, G.E., Wang, T. and Jiang, Y.
 TITLE Compounds for immunotherapy and diagnosis of colon cancer and
 methods for their use
 JOURNAL Patent: WO 0149716-A 245 12-JUL-2001;
 CORIXA CORPORATION (US)
 FEATURES Location/Qualifiers
 source 1. .508
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"
 ORIGIN
 Query Match 61.6%; Score 499; DB 6; Length 508;
 Best Local Similarity 100.0%; Pred. No. 6.9e-123;
 Matches 499; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 312 CGAGGAGTCGCTTAAGTGCAGGGACCTCAAAGTGGACAATATATTGTAAAGATCCAAA 371
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 Qy 372 AATAAATGACGCTACGCAAGAACCACTAACAGTTAACGTACAAACTACACAGCTCATGTTCTG 431
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 Qy 792 AACGCAATTATATCCATAA 810
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 Db 481 AACGCAATTATATCCATAA 499

RESULT 11
 AF353993
 LOCUS AF353993 630 bp mRNA linear ROD 29-MAY-2001
 DEFINITION Mus musculus beta-amyloid binding protein (Bbp) mRNA, complete cds.

ACCESSION AF353993
 VERSION AF353993.1 GI:13625464
 KEYWORDS .
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 630)
 AUTHORS Kajkowski,E.M., Lo,C.F., Ning,X., Walker,S., Sofia,H.J., Wang,W.,
 Edris,W., Chanda,P., Wagner,E., Vile,S., Ryan,K.,
 McHendry-Rinde,B., Smith,S.C., Wood,A., Rhodes,K.J., Kennedy,J.D.,
 Bard,J., Jacobsen,J.S. and Ozenberger,B.A.
 TITLE beta -Amyloid peptide-induced apoptosis regulated by a novel
 protein containing a g protein activation module
 JOURNAL J. Biol. Chem. 276 (22), 18748-18756 (2001)
 MEDLINE 21276355
 PUBMED 11278849
 REFERENCE 2 (bases 1 to 630)
 AUTHORS Ozenberger,B.A., Howland,D.S., Lo,C.F. and She,Y.
 TITLE Direct Submission
 JOURNAL Submitted (27-FEB-2001) Wyeth Neuroscience, CN 8000, Princeton, NJ
 08543, USA
 FEATURES Location/Qualifiers
 source 1. .630
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="BALB/c"
 /db_xref="taxon:10090"
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 /gene="Bbp"
 CDS 4. .630
 /gene="Bbp"
 /note="integral membrane glycoprotein"
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 /db_xref="GI:13625465"
 /translation="MAAAWPAGRASPAAGPPGLRTLWLVTVAGHC GAAASGAVGGE
 ETPKCEDLRVGQYICKEPKINDATQE PVNCTNYTAHVQCFPAPKITCKDLSGNETHFT
 GSEVGFLKPISCRNVNGSYKVAVALSLFLGWLGA DRFYLGYPALGLLKFCTVGF CGI
 GSLIDFILISMQIVGP SDGSSYIIDYYGTRLRLSITNETFRKTQLYP"
 misc_feature 349. .414
 /gene="Bbp"
 /note="Region: transmembrane domain"
 misc_feature 457. .528
 /gene="Bbp"
 /note="Region: transmembrane domain"

ORIGIN

Query Match 58.2%; Score 471.6; DB 10; Length 630;
 Best Local Similarity 85.4%; Pred. No. 1.6e-115;
 Matches 538; Conservative 0; Mismatches 89; Indels 3; Gaps 1;

 Qy 184 AAGATGGCGGCCGCCTGGCCGTCTGGTCCGTCTGCTCCGGAGGCCGTGACGCCAGACTC 243
 ||||||| ||||| ||||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| |
 Db 1 AACATGGCGGCCGCCTGGCCCGCGGGCTTCCCCAGCGGGGGCCTCCGGGCCTT 60

Qy	244	GTTGGTGCCTGTGGTCGTCAGTCACTACAGGACCCGGGGCTGGGCCAC---C	300
Db	61	CTCCGCACCCTGTGGCTCGTGACGGTCGCCGGACACTGTGGGCTGCTGCCTCTGGC	120
Qy	301	TCCGCCGGGGCGAGGAGTCGCTTAAGTGCAGGACCTCAAAGTGGACAATATATTGT	360
Db	121	GCTGTCGGGGCGAGGAGACACCCAAGTGTGAGGACCTCAGGGTGGGACAATATATTGT	180
Qy	361	AAAGATCCAAAATAATGACGCTACGCAAGAACAGTTAAGTACAAACTACACAGCT	420
Db	181	AAAGAACCAAAAATAATGATGCTACGCAAGAACAGTTAATTGTACAAACTACACAGCT	240
Qy	421	CATGTTCCCTGTTCCAGCACCCAACATAACTTGTAAAGGATTCCAGTGGCAATGAAACA	480
Db	241	CATGTTCAATGTTCCAGCACCCAAAATAACTTGTAAAGGATTGAGTGGTAATGAAACA	300
Qy	481	CATTTACTGGAACGAAGTGGTTTTCAAGCCATATCTTGGCAAATGTAAATGGC	540
Db	301	CATTTACTGGAACGTGAAGTCGGTTTCTCAAGCCATATCTTGGCAAATGTAAATGGC	360
Qy	541	TATT CCTACAAAGTGGCAGTCGATTGTCCTTTCTTGGATGGTTGGAGCAGATCGA	600
Db	361	TATT CGTACAAAGTGGCAGTTGCATTATCTCTTTGGATGGCTGGAGCAGATCGA	420
Qy	601	TTTTACCTGGATACCTGCTTGGTTGTTAAAGTTTGCAGTGTAGGGTTGTGGA	660
Db	421	TTTTACCTCGGATATCCTGCCTTAGGCTGTTAAATTTGCACCGTAGGATTGCGGA	480
Qy	661	ATTGGGAGCCTAATTGATTCATTCTTATTCATGCAGATTGTTGGACCTTCAGATGGA	720
Db	481	ATTGGGAGCCTAATTGATTCATTCTTATTCATGCAGATTGTTGGACCTTCAGATGGA	540
Qy	721	AGTAGTTACATTAGATTACTATGGAACCAGACTACAAGACTGAGTATTACTAATGAA	780
Db	541	AGTAGTTACATTAGACTATTATGGAACCAGGCTACAAGACTCAGCATTACTAATGAA	600
Qy	781	ACATTAGAAAAACGCAATTATCCATAA	810
Db	601	ACATTAGAAAAACCCAGCTGTACCCATAA	630

RESULT 12

BD076181

LOCUS BD076181 440 bp DNA linear PAT 27-AUG-2002
DEFINITION 5' EST of tissue-nonspecific secretory protein.
ACCESSION BD076181
VERSION BD076181.1 GI:22621784
KEYWORDS JP 2001512011-A/129.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 440)
AUTHORS Edwards, J.B.D.M., Duclert, A. and Lacroix, B.
TITLE 5' EST of tissue-nonspecific secretory protein
JOURNAL Patent: JP 2001512011-A 129 21-AUG-2001;
GENSET

COMMENT OS Homo sapiens (human)
PN JP 2001512011-A/129
PD 21-AUG-2001
PF 31-JUL-1998 JP 2000505289
PR 01-AUG-1997 US 08/905135
PI JEAN BAPTISTE DUMAS MILNE EDWARDS,AYMERIC DUCLERT,BRUNO PI
LACROIX
PC C12N15/09,C12N15/09,C07K14/47,C12Q1/68,C12N15/00,C12N15/00 CC
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CC identity 97
CC region 113. .315
CC id AA143062
CC est
CC blastn
CC identity 99
CC region 304. .411
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CC id N47594

CC est
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CC id HUM159G08B
CC est
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CC identity 95
CC region 1. .47
CC id HUM159G08B

CC est
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CC identity 98
CC region 92. .316
CC id N34957
CC est
CC blastn
CC identity 100
CC region 30. .97
CC id N34957
CC est
CC blastn
CC identity 91
CC region 312. .379
CC id N34957
CC est
CC Von Heijne matrix
CC score 8.7
CC seq AVALSLFLGWLGA/DR
FH Key Location/Qualifiers
FT misc_feature 143. .345
FT misc_feature 335. .442
FT misc_feature 72. .149
FT misc_feature 72. .345
FT misc_feature 372. .442
FT misc_feature 35. .73
FT misc_feature 153. .442
FT misc_feature 77. .147
FT misc_feature 72. .412
FT misc_feature 27. .73
FT misc_feature 143. .367
FT misc_feature 80. .147
FT misc_feature 362. .429
FT sig_peptide 24. .431.

FEATURES Location/Qualifiers
source 1. .440
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ORIGIN

Query Match 53.9%; Score 436.8; DB 6; Length 440;
Best Local Similarity 99.5%; Pred. No. 3.4e-106;
Matches 436; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY	166	GAGAAAGTGTGGTCTCCAAGATGGCGGCCCTGGCCGTCTGGTCCGTCTGCTCCGGAG	225
Db	3	GAGAAAGTGTGGTCTCCAAGATGGCGGCCCTGGCSDTCTGGTCCGTCTGCTCCGGAG	62
QY	226	GCCGTGACGCCAGACTCGTTGGTGTCCCTGTGGTCGTCTCAGTCACTACAGGACCTGG	285
Db	63	GCCGTGACGCCAGACTCGTTGGTGTCCCTGTGGTCGTCTCAGTCACTACAGGACCTGG	122
QY	286	GGGGCTGTTGCCACCTCCGCCGGGGCGAGGAGTCGCTTAAGTGCAGGACCTAAAGTG	345
Db	123	GGGGCTGTTGCCACCTCCGCCGGGGCGAGGAGTCGCTTAAGTGCAGGACCTAAAGTG	182

Qy	346 GGACAATATTTGTAAAGATCCAAAATAATGACGCTACGCAAGAACCGAGTTAAGTGT 405
Db	183 GGACAATATTTGTAAAGATCCAAAATAATGACGCTACGCAAGAACCGAGTTAAGTGT 242
Qy	406 ACAAACTACACAGCTCATGTTCCAGCACCCAACATAACTGTAAGGATTCC 465
Db	243 ACAAACTACACAGCTCATGTTCCAGCACCCAACATAACTGTAAGGATTCC 302
Qy	466 AGTGGCAATGAAACACATTTACTGGAACGAAGTGGTTTTCAAGCCATATCTTGC 525
Db	303 AGTGGCAATGAAACACATTTACTGGAACGAAGTGGTTTTCAAGCCATATCTTGC 362
Qy	526 CGAAATGTAAATGGCTATTCTACAAAGTGGCAGTCGCATTGTCCTTTCTGGATGG 585
Db	363 CGAAATGTAAATGGCTATTCTACAAAGTGGCAGTCGCATTGTCCTTTCTGGATGG 422
Qy	586 TTGGGAGCAGATCGATT 603
Db	423 TTGGGAGCAGATCGATT 440

RESULT 13

AC102262/c

LOCUS AC102262 193660 bp DNA linear HTG 27-FEB-2003
 DEFINITION Mus musculus clone RP24-216B4, WORKING DRAFT SEQUENCE, 9 unordered pieces.
 ACCESSION AC102262
 VERSION AC102262.3 GI:28570462
 KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 193660)
 AUTHORS Birren,B., Nusbaum,C. and Lander,E.
 TITLE Mus musculus, clone RP24-216B4
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 193660)
 AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
 Anderson,S., Barna,N., Bastien,V., Boguslavkiy,L., Boukhalter,B.,
 Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B.,
 Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cook,A.,
 Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S.,
 Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S.,
 Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N.,
 Hagos,B., Heaford,A., Horton,L., Hulme,W., Iliev,I., Johnson,R.,
 Jones,C., Kamat,A., Karatas,A., Kells,C., LaRocque,K.,
 Lamazares,R., Landers,T., Lehoczky,J., Levine,R., Liu,G.,
 MacLean,C., Macdonald,P., Major,J., Marquis,N., Matthews,C.,
 McCarthy,M., McEwan,P., McKernan,K., McPheevers,R., Meldrim,J.,
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 Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D.,
 Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V.,
 Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P.,
 Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupback,R.,
 Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
 Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,

Topham,K., Travers,M., Travis,N., Trigilio,J., Vassiliev,H.,
 Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
 Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
TITLE Direct Submission
JOURNAL Submitted (23-NOV-2001) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
REFERENCE 3 (bases 1 to 193660)
AUTHORS Birren,B., Nusbaum,C., Lander,E., Abouelleil,A., Allen,N.,
 Anderson,S., Arachchi,H.M., Barna,N., Bastien,V., Bloom,T.,
 Boguslavkiy,L., Boukhgalter,B., Camarata,J., Chang,J., Choepel,Y.,
 Collymore,A., Cook,A., Cooke,P., Corum,B., DeArellano,K.,
 Diaz,J.S., Dodge,S., Dooley,K., Dorris,L., Erickson,J., Faro,S.,
 Ferreira,P., FitzGerald,M., Gage,D., Galagan,J., Gardyna,S.,
 Graham,L., Grand-Pierre,N., Hafez,N., Hagopian,D., Hagos,B.,
 Hall,J., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C.,
 Kamat,A., Karatas,A., Kells,C., Landers,T., Levine,R.,
 Lindblad-Toh,K., Liu,G., Lui,A., Mabbitt,R., MacLean,C.,
 Macdonald,P., Major,J., Manning,J., Matthews,C., McCarthy,M.,
 Meldrim,J., Meneus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J.,
 Nguyen,C., Nicol,R., Norbu,C., O'Connor,T., O'Donnell,P.,
 O'Neil,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N.,
 Rachupka,A., Ramasamy,U., Raymond,C., Retta,R., Rise,C., Rogov,P.,
 Roman,J., Schauer,S., Schupback,R., Seaman,S., Severy,P., Smith,C.,
 Spencer,B., Stange-Thomann,N., Stojanovic,N., Stubbs,M.,
 Talamas,J., Tesfaye,S., Theodore,J., Topham,K., Travers,M.,
 Vassiliev,H., Venkataraman,V.S., Viel,R., Vo,A., Wilson,B., Wu,X.,
 Wyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
TITLE Direct Submission
JOURNAL Submitted (27-FEB-2003) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
COMMENT On Feb 27, 2003 this sequence version replaced gi:22381123.
 All repeats were identified using RepeatMasker:
 Smit, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>
----- Genome Center
 Center: Whitehead Institute/ MIT Center for Genome Research
 Center code: WIBR
 Web site: <http://www-seq.wi.mit.edu>
 Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
 Center project name: L18275
 Center clone name: 216_B_4
----- Summary Statistics
 Sequencing vector: Plasmid; n/a; 100% of reads
 Chemistry: Dye-terminator Big Dye; 100% of reads
 Assembly program: Phrap; version 0.960731
 Consensus quality: 191505 bases at least Q40
 Consensus quality: 192178 bases at least Q30
 Consensus quality: 192605 bases at least Q20
 Insert size: 188000; agarose-fp
 Insert size: 192860; sum-of-contigs
 Quality coverage: 10.3 in Q20 bases; agarose-fp
 Quality coverage: 10.0 in Q20 bases; sum-of-contigs

 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 9 contigs. The true order of the pieces
 * is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 16245: contig of 16245 bp in length
* 16246 16345: gap of 100 bp
* 16346 17545: contig of 1200 bp in length
* 17546 17645: gap of 100 bp
* 17646 21998: contig of 4353 bp in length
* 21999 22098: gap of 100 bp
* 22099 31133: contig of 9035 bp in length
* 31134 31233: gap of 100 bp
* 31234 41801: contig of 10568 bp in length
* 41802 41901: gap of 100 bp
* 41902 62223: contig of 20322 bp in length
* 62224 62323: gap of 100 bp
* 62324 91590: contig of 29267 bp in length
* 91591 91690: gap of 100 bp
* 91691 123816: contig of 32126 bp in length
* 123817 123916: gap of 100 bp
* 123917 193660: contig of 69744 bp in length.

FEATURES Location/Qualifiers

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/db_xref="taxon:10090"
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vector_side:right"

ORIGIN

Query Match 53.2%; Score 430.6; DB 2; Length 193660;
Best Local Similarity 81.7%; Pred. No. 5.2e-104;
Matches 535; Conservative 0; Mismatches 114; Indels 6; Gaps 3;

RESULT 14
BD076249

LOCUS BD076249 455 bp DNA linear PAT 27-AUG-2002
DEFINITION 5' EST of tissue-nonspecific secretory protein.
ACCESSION BD076249
VERSION BD076249.1 GI:22621852
KEYWORDS JP 2001512011-A/197.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 455)
AUTHORS Edwards,J.B.D.M., Duclert,A. and Lacroix,B.
TITLE 5' EST of tissue-nonspecific secretory protein
JOURNAL Patent: JP 2001512011-A 197 21-AUG-2001;
GENSET
COMMENT OS Homo sapiens (human)
PN JP 2001512011-A/197
PD 21-AUG-2001
PF 31-JUL-1998 JP 2000505289
PR 01-AUG-1997 US 08/905135
PI JEAN BAPTISTE DUMAS MILNE EDWARDS,AYMERIC DUCLERT, BRUNO PI
LACROIX
PC C12N15/09,C12N15/09,C07K14/47,C12Q1/68,C12N15/00,C12N15/00 CC
blastn
CC identity 99
CC region 125. .358
CC id N47594
CC est
CC blastn
CC identity 100
CC region 49. .119
CC id N47594
CC est
CC blastn
CC identity 96
CC region 374. .438
CC id N47594
CC est
CC blastn
CC identity 96
CC region 113. .315
CC id AA143062
CC est
CC blastn
CC identity 97
CC region 43. .120
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CC est
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CC identity 98
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CC id AA143062
CC est
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CC est

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CC region 44. .317
CC id HUM172D06B
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CC identity 97
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CC est
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CC est
CC blastn
CC identity 97
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CC est
CC blastn
CC identity 98
CC region 92. .316
CC id N34957
CC est
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CC identity 100
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CC id N34957
CC est
CC Von Heijne matrix
CC score 5.5
CC seq LVGVLFVSVTTG/PW
CC n=a, g, c or t

FH	Key	Location/Qualifiers
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FT	misc_feature	60. .333
FT	misc_feature	388. .434
FT	misc_feature	23. .61
FT	misc_feature	60. .374
FT	misc_feature	15. .61
FT	misc_feature	131. .355
FT	misc_feature	68. .135
FT	sig_peptide	12. .104
FT	misc_feature	288
FT	misc_feature	375. .376

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ORIGIN

Query Match 52.5%; Score 425.2; DB 6; Length 455;
 Best Local Similarity 96.3%; Pred. No. 4.5e-103;
 Matches 439; Conservative 3; Mismatches 12; Indels 2; Gaps 1;

Qy	177 GGTCTCCAAGATGGCGGCCCTGGCGTCTGGTCCGTCTGCTCCGGAGGCCGTGACGGC 236
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Db	2 GGTCTCCAAGATGGCGGCCCTGGCGTCTGGTCCGTCTGCTCCGGAGGCCGTGACGGC 61
Qy	237 CAGACTCGTTGGTGTCCGTGGTCAGTCAGTCACTACAGGACCTGGGGGCTGTTGC 296
Db	62 CAGACTCGTTGGTGTCCGTGGTCAGTCAGTCACTACAGGACCTGGGGGCTGTTGC 121
Qy	297 CACCTCCGCCGGGGCGAGGAGTCGCTTAAGTGCAGGACCTAAAGTGGACAATATAT 356
Db	122 CACCTCCGCCGGGGCGAGGAGTCGCTTAAGTGCAGGACCTAAAGTGGACAATATAT 181
Qy	357 TTGTAAAGATCCAAAATAATGACGCTACGCAAGAACAGTTAAGTACAAACTACAC 416
Db	182 TTGTAAAGATCCAAAATAATGACGCTACGCAAGAACAGTTAAGTACAAACTACAC 241
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Db	242 AGCTCATTTCCGTGGCAGCACCAACATAACTTGTAAGGATNCCAGTGGCAATGA 301
Qy	477 AACACATTTACTGGGAACGAAGTTGGTTTTCAAGCCCATACTTGCAGGAAATGTAAA 536
Db	302 AACACATTTACTGGGAACGAAGTTGGTTTTCAAGCCCATACTTGCAGGAAATGTAAA 361
Qy	537 TGGCTATTCCCTACAAAGTGGCAGTCGCATTGTCTCTTTCTGGATGGTGGAGCAGA 596
	:
Db	362 TGGCTATTCCCTAC--NNTKAGCAGTNNTGTCTCTTTCTGGATGGTGGAGCAGA 419
Qy	597 TCGATTTACCTTGGATACCCTGCTTGGTTGTT 632
Db	420 TCGATTTACCTTGGATACCCTGCTTGGTTGTT 455

RESULT 15

AX892343

LOCUS	AX892343	487 bp	DNA	linear	PAT 18-DEC-2003
DEFINITION	Sequence 8206 from Patent EP1033401.				
ACCESSION	AX892343				
VERSION	AX892343.1 GI:40047227				
KEYWORDS	.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE	1				

Search completed: March 4, 2004, 08:34:00
Job time : 3291 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 4, 2004, 03:41:27 ; Search time 385 Seconds
(without alignments)
8937.767 Million cell updates/sec

Title: US-09-852-100B-1

Perfect score: 810

Sequence: 1 atgcatatttaaaagggtc.....aaacgcaattatatccataa 810

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_29Jan04:
1: geneseqn1980s:
2: geneseqn1990s:
3: geneseqn2000s:
4: geneseqn2001as:
5: geneseqn2001bs:
6: geneseqn2002s:
7: geneseqn2003as:
8: geneseqn2003bs:
9: geneseqn2003cs:
10: geneseqn2004s:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result	Query					Description
No.	Score	Match	Length	DB	ID	
1	810	100.0	810	2	AAX05735	Aax05735 Human bet
2	810	100.0	810	3	AAZ52369	Aaz52369 Human bet
3	810	100.0	810	7	AAD51940	Aad51940 Human BBP
4	810	100.0	1246	7	AAD51979	Aad51979 Human BBP
5	602.8	74.4	970	2	AAX97705	Aax97705 Extended
6	499	61.6	508	3	AAA77946	Aaa77946 cDNA enco
7	499	61.6	508	3	AAA77958	Aaa77958 cDNA enco
8	499	61.6	508	4	AAI28684	Aai28684 Colon tum

9	499	61.6	508	4	AAI28696	Aai28696	Colon tum
10	499	61.6	508	7	ABZ32882	Abz32882	Human col
11	499	61.6	508	7	ABZ32870	Abz32870	Human col
12	442.2	54.6	1095	6	ABK52558	Abk52558	cDNA enco
13	436.8	53.9	440	2	AAX41191	Aax41191	Human sec
14	425.2	52.5	455	2	AAX41259	Aax41259	Human sec
15	411.4	50.8	487	3	AAC04131	Aac04131	Human sec
16	337.4	41.7	431	8	ACH19706	Ach19706	Human adu
17	322	39.8	323	7	ACD92727	Acd92727	Human col
18	320.4	39.6	323	7	ACD92728	Acd92728	Human col
c 19	182.4	22.5	561	6	ABQ57089	Abq57089	Human col
20	153.2	18.9	515	9	ADB56631	Adb56631	Toxicity-
21	115.4	14.2	433	5	ABV17809	Abv17809	Human pro
22	115.4	14.2	487	5	ABV47601	Abv47601	Human pro
23	113	14.0	292	7	AAD51978	Aad51978	Human BBP
24	99.8	12.3	298	2	AAX85735	Aax85735	Novel cDN
c 25	64.6	8.0	2771	4	ABL16838	Ab116838	Drosophil
c 26	64.6	8.0	3642	4	ABL15742	Ab115742	Drosophil
27	64.4	8.0	706	4	ABL16839	Ab116839	Drosophil
28	51	6.3	1369	2	AAX85024	Aax85024	Human sec
29	51	6.3	1369	7	ADA56147	Ada56147	Gene enco
30	51	6.3	1369	7	ACD18950	Acd18950	Novel hum
31	51	6.3	1369	7	ACC50529	Acc50529	Human sec
32	51	6.3	1369	7	ABZ71291	Abz71291	Secreted
33	51	6.3	1369	8	ADB91205	Adb91205	Human sec
34	51	6.3	1369	9	ADC73589	Adc73589	Human sec
35	50.4	6.2	690	3	AAA64413	Aaa64413	Open read
36	50.4	6.2	854	3	AAA64412	Aaa64412	DNA encod
c 37	50.2	6.2	439	6	ABK62922	Abk62922	Rat seque
c 38	50.2	6.2	439	9	ADB56953	Adb56953	Toxicity-
39	49.8	6.1	741	3	AAA64409	Aaa64409	Open read
40	49.8	6.1	746	3	AAZ52371	Aaz52371	Human bet
41	49.8	6.1	1406	7	ACC51100	Acc51100	Human Amy
42	49.8	6.1	1455	4	AAF80523	Aaf80523	Receptor
43	49.8	6.1	1473	3	AAA64408	Aaa64408	DNA encod
44	49.8	6.1	1473	3	AAA64425	Aaa64425	DNA encod
45	49.8	6.1	1473	3	AAA64424	Aaa64424	DNA encod

ALIGNMENTS

RESULT 1
AAX05735
ID AAX05735 standard; mRNA; 810 BP.
XX
AC AAX05735;
XX
DT 27-APR-1999 (first entry)
XX
DE Human beta-amyloid peptide-binding protein (BBP) encoding mRNA.
XX
KW Beta-amyloid peptide binding protein; BBP; beta-amyloid protein; BAP;
KW human; Alzheimer's disease; ss.
XX
OS Homo sapiens.
XX

FH Key Location/Qualifiers
FT CDS 1..810
FT /*tag= a
FT /product= "BBP"
XX
PN WO9846636-A2.
XX
PD 22-OCT-1998.
XX
PF 14-APR-1998; 98WO-US007462.
XX
PR 16-APR-1997; 97US-0064583P.
XX
PA (AMHP) AMERICAN HOME PROD CORP.
XX
PI Ozenberger BA, Kajkowski EM, Jacobsen JS, Bard JA, Walker SG;
XX
DR WPI; 1999-080736/07.
DR P-PSDB; AAW94291.
XX
PT Polynucleotide encoding beta-amyloid peptide binding protein - used to
PT identify inhibitors of beta-amyloid peptide for treating Alzheimer's
PT disease.
XX
PS Claim 1; Page 43-44; 59pp; English.
XX
CC This represents a nucleotide sequence encoding a beta-amyloid peptide
CC binding protein (BBP). The polynucleotide comprising the entire BBP
CC nucleotide sequence of clone BBP1-f1 is deposited under the accession
CC number ATCC 98617. The polynucleotide comprising a fragment of BBP
CC (nucleotides 202-807 of the full length BBP) of clone PEK196 is deposited
CC as ATCC 98399. Host cells transformed with a vector comprising the BBP
CC nucleic acid are used for the recombinant production of the protein. The
CC protein can be used in a method for diagnosing a disease characterised by
CC aberrant expression of human beta-amyloid protein (BAP). The protein can
CC also be used in a method for screening for compounds which regulate
CC expression of a BAP binding protein. The proteins, antibodies and
CC identified compounds can be used in the treatment or prevention of
CC Alzheimer's disease
XX
SQ Sequence 810 BP; 204 A; 183 C; 202 G; 221 T; 0 U; 0 Other;

Query Match 100.0%; Score 810; DB 2; Length 810;
Best Local Similarity 100.0%; Pred. No. 2e-233;
Matches 810; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGCATATTTAAAAGGGTCTCCCAATGTGATTCCACGGGCTCACGGGCAGAACACAGG 60
Db 1 ATGCATATTTAAAAGGGTCTCCCAATGTGATTCCACGGGCTCACGGGCAGAACACG 60

Qy 61 CGAAGAGACGGAACTGGCCTCTATCCTATGCGAGGTCCCTTAAGAACCTGCCCTGTTG 120
Db 61 CGAAGAGACGGAACTGGCCTCTATCCTATGCGAGGTCCCTTAAGAACCTGCCCTGTTG 120

Qy 121 CCCTTCTCCCTCCGCTCCTGGCGGAGGCGGAAGCGGAAGTGGCGAGAAAGTGTGGTC 180
Db 121 CCCTTCTCCCTCCGCTCCTGGCGGAGGCGGAAGCGGAAGTGGCGAGAAAGTGTGGTC 180

Qy	181	TCCAAGATGGCGGCCGCTGGCCGTCTGGTCGTCTGCCGGAGGCCGTACGCCAGA	240
Db	181	TCCAAGATGGCGGCCGCTGGCCGTCTGGTCGTCTGCCGGAGGCCGTACGCCAGA	240
Qy	241	CTCGTTGGTGCCTGTGGTCGTCTCAGTCACTACAGGACCTGGGGGCTGTTGCCACC	300
Db	241	CTCGTTGGTGCCTGTGGTCGTCTCAGTCACTACAGGACCTGGGGGCTGTTGCCACC	300
Qy	301	TCCGCCGGGGCGAGGAGTCGCTTAAGTGCGAGGACCTCAAAGTGGACAATATATTGT	360
Db	301	TCCGCCGGGGCGAGGAGTCGCTTAAGTGCGAGGACCTCAAAGTGGACAATATATTGT	360
Qy	361	AAAGATCCAAAATAATGACGCTACGCAAGAACAGTTAAGTACAAACTACACAGCT	420
Db	361	AAAGATCCAAAATAATGACGCTACGCAAGAACAGTTAAGTACAAACTACACAGCT	420
Qy	421	CATTTCCCTGTTTCCAGCACCCAACATAACTGTAAGGATTCCAGTGGCAATGAAACA	480
Db	421	CATTTCCCTGTTTCCAGCACCCAACATAACTGTAAGGATTCCAGTGGCAATGAAACA	480
Qy	481	CATTTACTGGAACGAAGTTGGTTTTCAAGCCCATACTTGATGGGAGCAGATCGA	540
Db	481	CATTTACTGGAACGAAGTTGGTTTTCAAGCCCATACTTGATGGGAGCAGATCGA	540
Qy	541	TATTCCCTACAAAGTGGCAGTCGATTGTCTCTTTCTGGATGGTGGAGCAGATCGA	600
Db	541	TATTCCCTACAAAGTGGCAGTCGATTGTCTCTTTCTGGATGGTGGAGCAGATCGA	600
Qy	601	TTTACCTGGATACCTGCTTGGTTGTTAAAGTTGCACTGTAGGGTTGTGGA	660
Db	601	TTTACCTGGATACCTGCTTGGTTGTTAAAGTTGCACTGTAGGGTTGTGGA	660
Qy	661	ATTGGGAGCCTAATTGATTCATTCTATTCAATGCAGATTGGACCTTCAGATGGA	720
Db	661	ATTGGGAGCCTAATTGATTCATTCTATTCAATGCAGATTGGACCTTCAGATGGA	720
Qy	721	AGTAGTTACATTATAGATTACTATGGAACCAGACTTACAAGACTGAGTATTACTAATGAA	780
Db	721	AGTAGTTACATTATAGATTACTATGGAACCAGACTTACAAGACTGAGTATTACTAATGAA	780
Qy	781	ACATTTAGAAAAACGCAATTATATCCATAA	810
Db	781	ACATTTAGAAAAACGCAATTATATCCATAA	810

RESULT 2

AAZ52369

ID AAZ52369 standard; cDNA; 810 BP.

XX

AC AAZ52369;

XX

DT 24-JUL-2000 (first entry)

XX

DE Human beta-amyloid peptide (BAP) binding protein, BBP1 encoding cDNA.

XX

KW Beta-amyloid peptide binding protein; BBP; BAP; tumour; suppressor;

KW G-protein coupled receptor; GPCR; integral membrane protein; antigen;
KW neuronal cell; nonhuman primate; NHP; G-protein signalling pathway;
KW apoptosis; immunogen; therapeutic; treatment; prevention; diagnostic; ss.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT CDS 1. .810

FT /*tag= a

FT /product= "Human BBP1 protein"

FT /note= "Member of G-protein coupled receptor superfamily"

XX

PN WO200022125-A2.

XX

PD 20-APR-2000.

XX

PF 13-OCT-1999; 99WO-US021621.

XX

PR 13-OCT-1998; 98US-0104104P.

XX

PA (AMHP) AMERICAN HOME PROD CORP.

XX

PI Ozenberger BA, Kajkowski EM, Lo CF;

XX

DR WPI; 2000-317982/27.

DR P-PSDB; AAY70759.

XX

PT Novel G-protein-coupled receptor-like proteins and polynucleotides useful
PT for regulating apoptosis, comprises integral membrane protein traversing
PT the membrane twice.

XX

PS Example 1; Page 60-61; 68pp; English.

XX

CC The present sequence is the cDNA encoding beta-amyloid peptide (BAP)
CC binding protein-1 (BBP1). It is an integral membrane protein, that
CC traverse the membrane twice. It is related to G protein-coupled receptor
CC (GPCR) protein superfamily. It interacts with G-alpha proteins and
CC regulates the activity of G-protein signalling pathways. BBP genes are
CC widely expressed in neuronal cells of nonhuman primate (NHP) brain and
CC overexpressed in some tumours. It functions as a suppressor of apoptosis
CC induction. BBP proteins are used as immunogens to raise antibodies,
CC useful as therapeutics and as antigens in solid phase assays. They are
CC also useful as reagents to identify molecules which effect the
CC interaction of BBP and a cloned protein, that are useful in the treatment
CC or prevention of diseases associated with apoptosis. The polynucleotides
CC are useful for diagnostics. Note: In claim 5, the patent claims an amino
CC acid sequence from figure 2. However, figure 2 does not contain any
CC sequence. It is inferred from the disclosure that the figure 2 sequence
CC refers to BBP1 protein, encoded by this polynucleotide sequence

XX

SQ Sequence 810 BP; 204 A; 183 C; 202 G; 221 T; 0 U; 0 Other;

Query Match 100.0%; Score 810; DB 3; Length 810;

Best Local Similarity 100.0%; Pred. No. 2e-233;

Matches 810; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGCATATTAAAAGGGTCTCCAATGTGATTCCACGGGCTCACGGGCAGAAGAACACG 60

Db	1	ATGCATATTAAAAGGGTCTCCAATGTGATTCCACGGGCTCACGGCAGAAGAACACG	60
Qy	61	CGAAGAGACGGAACTGGCCTCTATCCTATGCAGGTCCCTTAAGAACCTGCCCTGTTG	120
Db	61	CGAAGAGACGGAACTGGCCTCTATCCTATGCAGGTCCCTTAAGAACCTGCCCTGTTG	120
Qy	121	CCCTCTCCCTCCGCTCCTGGCGAGGCGGAAGCGGAAGTGGCGAGAAAGTGTGGTC	180
Db	121	CCCTCTCCCTCCGCTCCTGGCGAGGCGGAAGCGGAAGTGGCGAGAAAGTGTGGTC	180
Qy	181	TCCAAGATGGCGGCCCTGGCGTCTGGTCCGTCTGCTCCGGAGGCCGTACGCCAGA	240
Db	181	TCCAAGATGGCGGCCCTGGCGTCTGGTCCGTCTGCTCCGGAGGCCGTACGCCAGA	240
Qy	241	CTCGTTGGTGTCCGTGGTCAGTCAGTCACTACAGGACCTGGGGGCTGTTGCCACC	300
Db	241	CTCGTTGGTGTCCGTGGTCAGTCAGTCACTACAGGACCTGGGGGCTGTTGCCACC	300
Qy	301	TCCGCCGGGGCGAGGAGTCGCTTAAGTGCAGGACCTCAAAGTGGACAATATATTGT	360
Db	301	TCCGCCGGGGCGAGGAGTCGCTTAAGTGCAGGACCTCAAAGTGGACAATATATTGT	360
Qy	361	AAAGATCCAAAATAATGACGCTACGCAAGAACAGTTAAGTACAAACTACACAGCT	420
Db	361	AAAGATCCAAAATAATGACGCTACGCAAGAACAGTTAAGTACAAACTACACAGCT	420
Qy	421	CATTTCTGTTCCAGCACCAACATAACTTGTAAAGGATTCCAGTGGCAATGAAACA	480
Db	421	CATTTCTGTTCCAGCACCAACATAACTTGTAAAGGATTCCAGTGGCAATGAAACA	480
Qy	481	CATTTACTGGAACGAAGTGGTTTTCAAGCCCATACTTGTAAAGGATTCCAGTGGCAATGAAACA	540
Db	481	CATTTACTGGAACGAAGTGGTTTTCAAGCCCATACTTGTAAAGGATTCCAGTGGCAATGAAACA	540
Qy	541	TATTCTACAAAGTGGCAGTCGATTGCTCTTTCTTGATGGTGGAGCAGATCGA	600
Db	541	TATTCTACAAAGTGGCAGTCGATTGCTCTTTCTTGATGGTGGAGCAGATCGA	600
Qy	601	TTTACCTGGATACCTGCTTGGTTGTTAAAGTTGCAGTGTAGGGTTGTGGA	660
Db	601	TTTACCTGGATACCTGCTTGGTTGTTAAAGTTGCAGTGTAGGGTTGTGGA	660
Qy	661	ATTGGGAGCTAATTGATTCTTCAATGCAGATTGTGGACCTTCAGATGGA	720
Db	661	ATTGGGAGCTAATTGATTCTTCAATGCAGATTGTGGACCTTCAGATGGA	720
Qy	721	AGTAGTTACATTAGATTACTATGGAACCAGACTTACAAGACTGAGTATTACTAATGAA	780
Db	721	AGTAGTTACATTAGATTACTATGGAACCAGACTTACAAGACTGAGTATTACTAATGAA	780
Qy	781	ACATTTAGAAAAACGCAATTATATCCATAA	810
Db	781	ACATTTAGAAAAACGCAATTATATCCATAA	810

AAD51940
ID AAD51940 standard; cDNA; 810 BP.
XX
AC AAD51940;
XX
DT 02-MAY-2003 (first entry)
XX
DE Human BBP-1 cDNA.
XX
KW Human; beta-amyloid peptide-binding protein; BAP; Abeta; betaAP; BBP;
KW Alzheimer's disease; AD; transgenic; transgenic animal; gene therapy;
KW neuroprotective; nootropic; gene; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..810
FT /*tag= a
FT /product= "Human BBP-1"
XX
PN WO200290499-A2.
XX
PD 14-NOV-2002.
XX
PF 06-MAY-2002; 2002WO-US014223.
XX
PR 09-MAY-2001; 2001US-00852100.
XX
PA (AMHP) WYETH.
XX
PI Ozenberger BA, Bard JA, Kajkowski EM, Jacobsen JS, Walker SG;
PI Sofia HJ, Howland DS;
XX
DR WPI; 2003-120537/11.
DR P-PSDB; AAE33877.
XX
PT New human beta-amyloid peptide-binding protein, useful for diagnosing
PT and/or treating diseases associated with aberrant expression of beta-
PT amyloid peptide, e.g. Alzheimer's disease.
XX
PS Claim 1; Page 82-84; 85pp; English.
XX
CC The present invention relates to novel human beta-amyloid peptide (BAP;
CC Abeta, betaAP)-binding (BBP) proteins and polynucleotides encoding such
CC proteins. BBP sequences are useful to diagnose and/or treat diseases
CC associated with aberrant expression of human BAP such as Alzheimer's
CC disease (AD). They are used to generate transgenic animals. Sequences of
CC the invention are also used in gene therapy. The present sequence is
CC human BBP-1 cDNA
XX
SQ Sequence 810 BP; 204 A; 183 C; 202 G; 221 T; 0 U; 0 Other;

Query Match 100.0%; Score 810; DB 7; Length 810;
Best Local Similarity 100.0%; Pred. No. 2e-233;
Matches 810; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGCATATTAAAAGGGTCTCCAATGTGATTCCACGGGCTCACGGGCAGAAGAACACG 60

Db	1	ATGCATATTAAAAGGGTCTCCCAATGTGATTCCACGGGTCACGGGCAGAAGAACACG	60
Qy	61	CGAAGAGACGGAACTGGCCTCTATCCTATGCGAGGTCCCTTAAGAACCTGCCCTGTTG	120
Db	61	CGAAGAGACGGAACTGGCCTCTATCCTATGCGAGGTCCCTTAAGAACCTGCCCTGTTG	120
Qy	121	CCCTCTCCCTCCCGCTCCTGGCGGAGGCGAAGCGGAAGTGGCGAGAAAGTGTGGTC	180
Db	121	CCCTCTCCCTCCCGCTCCTGGCGGAGGCGAAGCGGAAGTGGCGAGAAAGTGTGGTC	180
Qy	181	TCCAAGATGGCGGCCGCCTGGCGCTGGTCCGCTGCTCCGGAGGCCGTGACGGCCAGA	240
Db	181	TCCAAGATGGCGGCCGCCTGGCGCTGGTCCGCTGCTCCGGAGGCCGTGACGGCCAGA	240
Qy	241	CTCGTTGGTGTCCGTGGTCCGTCACTACAGGACCTGGGGGCTGTTGCCACC	300
Db	241	CTCGTTGGTGTCCGTGGTCCGTCACTACAGGACCTGGGGGCTGTTGCCACC	300
Qy	301	TCCGCCGGGGCGAGGAGTCGCTTAAGTGCAGGACCTCAAAGTGGACAATATATTGT	360
Db	301	TCCGCCGGGGCGAGGAGTCGCTTAAGTGCAGGACCTCAAAGTGGACAATATATTGT	360
Qy	361	AAAGATCCAAAATAATGACGCTACGCAAGAACCAAGTTAACGTACAAACTACACAGCT	420
Db	361	AAAGATCCAAAATAATGACGCTACGCAAGAACCAAGTTAACGTACAAACTACACAGCT	420
Qy	421	CATTTCCCTGTTCCAGCACCAACATAACTGTAAGGATTCCAGTGGCAATGAAACA	480
Db	421	CATTTCCCTGTTCCAGCACCAACATAACTGTAAGGATTCCAGTGGCAATGAAACA	480
Qy	481	CATTTACTGGAACGAAGTTGGTTTTCAAGCCCATACTTGCGAAATGAAATGGC	540
Db	481	CATTTACTGGAACGAAGTTGGTTTTCAAGCCCATACTTGCGAAATGAAATGGC	540
Qy	541	TATTCTACAAAGTGGCAGTCGCATTGTCTCTTTCTGGATGGTGGAGCAGATCGA	600
Db	541	TATTCTACAAAGTGGCAGTCGCATTGTCTCTTTCTGGATGGTGGAGCAGATCGA	600
Qy	601	TTTACCTGGATACCTGCTTGGTTGTTAAAGTTGCACTGTAGGGTTGTGGA	660
Db	601	TTTACCTGGATACCTGCTTGGTTGTTAAAGTTGCACTGTAGGGTTGTGGA	660
Qy	661	ATTGGGAGCTAATTGATTCTTATTCATGCAATTGCAAGATTGGACCTTCAGATGGA	720
Db	661	ATTGGGAGCTAATTGATTCTTATTCATGCAATTGCAAGATTGGACCTTCAGATGGA	720
Qy	721	AGTAGTTACATTATAGATTACTATGGAACCAAGACTTACAAGACTGAGTATTACTAATGAA	780
Db	721	AGTAGTTACATTATAGATTACTATGGAACCAAGACTTACAAGACTGAGTATTACTAATGAA	780
Qy	781	ACATTTAGAAAAACGCAATTATATCCATAA	810
Db	781	ACATTTAGAAAAACGCAATTATATCCATAA	810

RESULT 4

AAD51979

ID AAD51979 standard; DNA; 1246 BP.

XX

AC AAD51979;

XX

DT 02-MAY-2003 (first entry)

XX

DE Human BBP-1 genomic DNA.

XX

KW Human; beta-amyloid peptide-binding protein; BAP; Abeta; betaAP; BBP;

KW Alzheimer's disease; AD; transgenic; transgenic animal; gene therapy;

KW neuroprotective; nootropic; ds.

XX

OS Homo sapiens.

XX

PN WO200290499-A2.

XX

PD 14-NOV-2002.

XX

PF 06-MAY-2002; 2002WO-US014223.

XX

PR 09-MAY-2001; 2001US-00852100.

XX

PA (AMHP) WYETH.

XX

PI Ozenberger BA, Bard JA, Kajkowski EM, Jacobsen JS, Walker SG;

PI Sofia HJ, Howland DS;

XX

DR WPI; 2003-120537/11.

XX

PT New human beta-amyloid peptide-binding protein, useful for diagnosing
PT and/or treating diseases associated with aberrant expression of beta-
PT amyloid peptide, e.g. Alzheimer's disease.

XX

PS Disclosure; Fig 11; 85pp; English.

XX

CC The present invention relates to novel human beta-amyloid peptide (BAP;
CC Abeta, betaAP)-binding (BBP) proteins and polynucleotides encoding such
CC proteins. BBP sequences are useful to diagnose and/or treat diseases
CC associated with aberrant expression of human BAP such as Alzheimer's
CC disease (AD). They are used to generate transgenic animals. Sequences of
CC the invention are also used in gene therapy. The present sequence is
CC human BBP-1 genomic DNA

XX

SQ Sequence 1246 BP; 318 A; 255 C; 283 G; 390 T; 0 U; 0 Other;

Query Match 100.0%; Score 810; DB 7; Length 1246;

Best Local Similarity 100.0%; Pred. No. 2.6e-233;

Matches 810; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGCATATTAAAAGGGTCTCCAATGTGATTCCACGGGCTCACGGGCAGAACACAG 60
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 118 ATGCATATTAAAAGGGTCTCCAATGTGATTCCACGGGCTCACGGGCAGAACACG 177

Qy 61 CGAAGAGACGGAACTGGCCTCTATCCTATGCGAGGTCCCTTAAGAACCTGCCCTGTTG 120
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 178 CGAAGAGACGGAACTGGCCTCTATCCTATGCGAGGTCCCTTAAGAACCTGCCCTGTTG 237

Qy	121	CCCTTCTCCCTCCGCTCCTGGCGGAGGCAGGAAGCGGAAGTGGCGAGAAAGTGTGGTC 180
Db	238	CCCTTCTCCCTCCGCTCCTGGCGGAGGCAGGAAGCGGAAGTGGCGAGAAAGTGTGGTC 297
Qy	181	TCCAAGATGGCGGCCGCCTGGCGTCTGGTCCGTCTGCTCCGGAGGCCGTGACGCCAGA 240
Db	298	TCCAAGATGGCGGCCGCCTGGCGTCTGGTCCGTCTGCTCCGGAGGCCGTGACGCCAGA 357
Qy	241	CTCGTTGGTGTCCCTGTGGTCGTCTCAGTCACTACAGGACCTGGGGGCTGTTGCCACC 300
Db	358	CTCGTTGGTGTCCCTGTGGTCGTCTCAGTCACTACAGGACCTGGGGGCTGTTGCCACC 417
Qy	301	TCCGCCGGGGCGAGGAGTCGCTTAAGTGCAGGACCTCAAAGTGGACAATATATTGT 360
Db	418	TCCGCCGGGGCGAGGAGTCGCTTAAGTGCAGGACCTCAAAGTGGACAATATATTGT 477
Qy	361	AAAGATCCAAAATAATGACGCTACGCAAGAACAGTTAACGTACAAACTACACAGCT 420
Db	478	AAAGATCCAAAATAATGACGCTACGCAAGAACAGTTAACGTACAAACTACACAGCT 537
Qy	421	CATGTTCCGTGTTCCAGCACCAACATAACTTGTAAAGGATTCCAGTGGCAATGAAACA 480
Db	538	CATGTTCCGTGTTCCAGCACCAACATAACTTGTAAAGGATTCCAGTGGCAATGAAACA 597
Qy	481	CATTTACTGGAACGAAAGTTGGTTTTCAAGCCCATACTTGCAAGGAAATGTAAATGGC 540
Db	598	CATTTACTGGAACGAAAGTTGGTTTTCAAGCCCATACTTGCAAGGAAATGTAAATGGC 657
Qy	541	TATT CCTACAAAGTGGCAGTCG CATT GTCTTTTCTGGATGGTGGAGCAGATCGA 600
Db	658	TATT CCTACAAAGTGGCAGTCG CATT GTCTTTTCTGGATGGTGGAGCAGATCGA 717
Qy	601	TTTTACCTGGATACCTGCTTGGTTTTGTTAAAGTTTGCAGTGTAGGGTTTGGA 660
Db	718	TTTTACCTGGATACCTGCTTGGTTTTGTTAAAGTTTGCAGTGTAGGGTTTGGA 777
Qy	661	ATTGGGAGCCTAATTGATTCATTCTTATTCAATGCAGATTGGACCTTCAGATGGA 720
Db	778	ATTGGGAGCCTAATTGATTCATTCTTATTCAATGCAGATTGGACCTTCAGATGGA 837
Qy	721	AGTAGTTACATTATAGATTACTATGGAACCAAGACTACAAGACTGAGTATTACTAATGAA 780
Db	838	AGTAGTTACATTATAGATTACTATGGAACCAAGACTACAAGACTGAGTATTACTAATGAA 897
Qy	781	ACATTAGAAAAACGCAATTATCCATAA 810
Db	898	ACATTAGAAAAACGCAATTATCCATAA 927

RESULT 5

AAX97705

ID AAX97705 standard; DNA; 970 BP.

XX

AC AAX97705;

XX

DT 13-SEP-1999 (first entry)

XX
DE Extended human secreted protein coding sequence, SEQ ID NO. 270.
XX
KW Secreted protein; human; cytokine; cellular proliferation; cell movement;
KW cellular differentiation; immune system regulator; anti-inflammatory;
KW haematopoiesis regulator; tissue growth regulator; tumour inhibitor;
KW reproductive hormone regulator; chemotaxis; chemokinesis; gene therapy;
KW genetic disease; ss.
XX
OS Homo sapiens.
XX
PN WO9931236-A2.
XX
PD 24-JUN-1999.
XX
PF 17-DEC-1998; 98WO-IB002122.
XX
PR 17-DEC-1997; 97US-0069957P.
PR 09-FEB-1998; 98US-0074121P.
PR 13-APR-1998; 98US-0081563P.
PR 10-AUG-1998; 98US-0096116P.
XX
PA (GEST) GENSET.
XX
PI Bougueret L, Duclert A, Dumas Milne Edwards J;
XX
DR WPI; 1999-385906/32.
DR P-PSDB; AAY36021.
XX
PT New isolated human secreted proteins.
XX
PS Claim 1; Page 346-347; 516pp; English.
XX
CC This sequence represents an extended human secreted protein coding
CC sequence of the invention. The secreted proteins can be used in treating
CC or controlling a variety of human conditions. The secreted proteins may
CC act as cytokines or may affect cellular proliferation or differentiation
CC or may act as immune system regulators, haematopoiesis regulators, tissue
CC growth regulators, regulators of reproductive hormones or cell movement
CC or have chemotactic/chemokinetic, receptor/ligand, anti-inflammatory or
CC tumour inhibition activity. The DNAs can be used in forensic procedures
CC to identify individuals or in diagnostic procedures to identify
CC individuals having genetic diseases resulting from abnormal expression of
CC the genes corresponding to the extended cDNAs. They are also useful for
CC constructing a high resolution map of the human chromosomes. They can
CC also be used for gene therapy to control or treat genetic diseases

XX
SQ Sequence 970 BP; 267 A; 173 C; 199 G; 323 T; 0 U; 8 Other;

Query Match 74.4%; Score 602.8; DB 2; Length 970;
Best Local Similarity 98.4%; Pred. No. 6.7e-171;
Matches 624; Conservative 5; Mismatches 3; Indels 2; Gaps 2;

Qy 177 GGTCTCCAAGATGGCGGCCGCTGGCCGTCTGGTCCGTCTGCTCCGGAGGCCGTGACGGC 236
||| ||| ||| ||| ||| ||| ||| ||| ||| :||| ||| ||| ||| |||
Db 2 GGTCTCCAAGATGGCGGCCGCTGGCCGTCTGGTCCGTCTGCTCCGGAGGCCGTGACGGC 61

Qy	237	CAGACTCGTTGGTGTCTGTGGTCGCTCAGTCACTA 	296
Db	62	CAGACTCGTTGGTGTCTGTGGTCGCTCAGTCACTA 	121
Qy	297	CACCTCCGCCGGGGCGAGGAGTCGCTTAAGTGC 	356
Db	122	CACCTCCGCCGGGGCGAGGAGTCGCTTAAGTGC 	181
Qy	357	TTGTAAAGATCCAAAATAAATGACGCTACGCAAGA 	416
Db	182	TTGTAAAGATCCAAAATAAATGACGCTACGCAAGA 	241
Qy	417	AGCTCATGTTCTGTTCCAGCACCCAACATAACT 	476
Db	242	AGCTCATGTTCTGTTCCAGCACCCAACATAACT 	301
Qy	477	AACACATTTACTGGAACGAAGTTGGTTTCAAGCC 	536
Db	302	AACACATTTACTGGAACGAAGTTGGTTTCAAGCC 	361
Qy	537	TGGCTATT CCTACAAAGTGGCAGTCGATTG 	596
Db	362	TGGCTATT CCTACAAATG-AGCAGTCGA-TG 	419
Qy	597	TCGATTTACCTGGATACCCTGCTTGGTTG 	656
Db	420	TCGATTTACCTGGATACCCTGCTTGGTTG 	479
Qy	657	TGGAATTGGGAGCCTAATTGATT 	716
Db	480	TGGAATTGGGAGCCTAATTGATT 	539
Qy	717	TGGAAGTAGTTACATTATAGATT 	776
Db	540	TGGAAGTAGTTACATTATAGATT 	599
Qy	777	TGAAACATTAGAAAAACGCAATT 	810
Db	600	TGAAACATTAGAAAAACGCAATT 	633

RESULT 6

AAA77946

ID AAA77946 standard; cDNA; 508 BP.

XX

AC AAA77946;

XX

DT 14-NOV-2000 (first entry)

XX

DE cDNA encoding human colon tumour polypeptide, SEQ ID NO:233.

XX

KW Human colon tumour polypeptide; tumour antigen; cancer; vaccine;
KW immunotherapy; diagnosis; progression; ss.

XX

OS Homo sapiens.

XX

PN WO200037643-A2.

XX
PD 29-JUN-2000.
XX
PF 23-DEC-1999; 99WO-US030909.
XX
PR 23-DEC-1998; 98US-00221298.
PR 02-JUL-1999; 99US-00347496.
PR 22-SEP-1999; 99US-00401064.
PR 19-NOV-1999; 99US-00444242.
PR 02-DEC-1999; 99US-00454150.
XX
PA (CORI-) CORIXA CORP.
XX
PI Xu J, Lodes MJ, Secrist H, Benson DR, Meagher MJ, Stolk J;
PI Wang T, Yuqiu J;
XX
DR WPI; 2000-442671/38.
XX
PT New colon tumor polypeptides used to inhibit the development of cancer,
PT especially colon cancer, and for diagnosing and monitoring the
PT progression of the cancer.
XX
PS Claim 1; Page 158-159; 229pp; English.
XX
CC Sequences AAA77722-A78199 represent 478 cDNAs encoding proteins or
CC portions of proteins which are associated with human colon tumours. The
CC invention also specifically discloses 8 human colon tumour proteins
CC (AAB11897-B11904). The nucleic acids, the polypeptides they encode, and
CC antigen presenting cells (APCs, preferably dendritic cells) expressing
CC such polypeptides may be used in vaccines that target tumour cells,
CC especially colon tumour cells, thereby inhibiting the development of
CC cancer. T-cells specific for the polypeptide expressed by the APC are
CC used to remove tumour cells from biological samples, especially blood or
CC fractions thereof. The sample or the isolated T-cells specific for the
CC polypeptide can then be used to inhibit cancer development. CD4+ and/or
CC CD8+ T-cells from a patient may be incubated with a polypeptide or
CC nucleic acid of the invention, or an APC expressing such a polypeptide,
CC to cause the proliferation of specific T-cells. The T-cells can be cloned
CC and then administered back to the patient to inhibit cancer development.
CC Nucleic acids encoding the polypeptides and antibodies against the
CC polypeptides may be used to determine the expression level of a tumour
CC protein of the invention, and therefore to determine whether cancer cells
CC are present. Such diagnostic methods may also be used to monitor the
CC progression of a cancer by repeating the processes at time intervals, and
CC comparing the current result to previous results. The present sequence
CC represents a cDNA encoding a human colon tumour polypeptide

XX
SQ Sequence 508 BP; 153 A; 89 C; 103 G; 163 T; 0 U; 0 Other;

Query Match 61.6%; Score 499; DB 3; Length 508;
Best Local Similarity 100.0%; Pred. No. 9.4e-140;
Matches 499; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 312 CGAGGAGTCGCTTAAGTGCAGGGACCTCAAAGTGGGACAATATTTGTAAAGATCCAAA 371
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 CGAGGAGTCGCTTAAGTGCAGGGACCTCAAAGTGGGACAATATTTGTAAAGATCCAAA 60

QY	372	AATAAATGACGCTACGCAAGAACCACTGTAACACTACACAGCTCATGTTCTG	431
Db	61	AATAAATGACGCTACGCAAGAACCACTGTAACACTACACAGCTCATGTTCTG	120
QY	432	TTTCCAGCACCCAACATAACTTGTAAAGGATTCCAGTGGCAATGAAACACATTACTGG	491
Db	121	TTTCCAGCACCCAACATAACTTGTAAAGGATTCCAGTGGCAATGAAACACATTACTGG	180
QY	492	GAACGAAGTTGGTTTTCAAGCCCATACTTGCGAAATGTAAATGGCTATTCTACAA	551
Db	181	GAACGAAGTTGGTTTTCAAGCCCATACTTGCGAAATGTAAATGGCTATTCTACAA	240
QY	552	AGTGGCAGTCGATTGTCTCTTTCTGGATGGTGGAGCAGATCGATTACCTTGG	611
Db	241	AGTGGCAGTCGATTGTCTCTTTCTGGATGGTGGAGCAGATCGATTACCTTGG	300
QY	612	ATACCCTGCTTGGTTGTTAAAGTTGCAGTGTAGGGTTTGTGGAATTGGAGCCT	671
Db	301	ATACCCTGCTTGGTTGTTAAAGTTGCAGTGTAGGGTTTGTGGAATTGGAGCCT	360
QY	672	AATTGATTCATTCTATTCAATGCAGATTGGACCTTCAGATGGAAGTAGTTACAT	731
Db	361	AATTGATTCATTCTATTCAATGCAGATTGGACCTTCAGATGGAAGTAGTTACAT	420
QY	732	TATAGATTACTATGGAACCAGACTTACAAGACTGAGTATTACTAATGAAACATTAGAAA	791
Db	421	TATAGATTACTATGGAACCAGACTTACAAGACTGAGTATTACTAATGAAACATTAGAAA	480
QY	792	AACGCAATTATATCCATAA	810
Db	481	AACGCAATTATATCCATAA	499

RESULT 7

AAA77958

ID AAA77958 standard; cDNA; 508 BP.

XX

AC AAA77958;

XX

DT 14-NOV-2000 (first entry)

XX

DE cDNA encoding human colon tumour polypeptide, SEQ ID NO:245.

XX

KW Human colon tumour polypeptide; tumour antigen; cancer; vaccine;

KW immunotherapy; diagnosis; progression; ss.

XX

OS Homo sapiens.

XX

PN WO200037643-A2.

XX

PD 29-JUN-2000.

XX

PF 23-DEC-1999; 99WO-US030909.

XX

PR 23-DEC-1998; 98US-00221298.

PR 02-JUL-1999; 99US-00347496.

PR 22-SEP-1999; 99US-00401064.

PR 19-NOV-1999; 99US-00444242.
PR 02-DEC-1999; 99US-00454150.
XX
PA (CORI-) CORIXA CORP.
XX
PI Xu J, Lodes MJ, Secrist H, Benson DR, Meagher MJ, Stolk J;
PI Wang T, Yuqiu J;
XX
DR WPI; 2000-442671/38.
XX
PT New colon tumor polypeptides used to inhibit the development of cancer,
PT especially colon cancer, and for diagnosing and monitoring the
PT progression of the cancer.
XX
PS Claim 1; Page 162; 229pp; English.
XX
CC Sequences AAA77722-A78199 represent 478 cDNAs encoding proteins or
CC portions of proteins which are associated with human colon tumours. The
CC invention also specifically discloses 8 human colon tumour proteins
CC (AAB11897-B11904). The nucleic acids, the polypeptides they encode, and
CC antigen presenting cells (APCs, preferably dendritic cells) expressing
CC such polypeptides may be used in vaccines that target tumour cells,
CC especially colon tumour cells, thereby inhibiting the development of
CC cancer. T-cells specific for the polypeptide expressed by the APC are
CC used to remove tumour cells from biological samples, especially blood or
CC fractions thereof. The sample or the isolated T-cells specific for the
CC polypeptide can then be used to inhibit cancer development. CD4+ and/or
CC CD8+ T-cells from a patient may be incubated with a polypeptide or
CC nucleic acid of the invention, or an APC expressing such a polypeptide,
CC to cause the proliferation of specific T-cells. The T-cells can be cloned
CC and then administered back to the patient to inhibit cancer development.
CC Nucleic acids encoding the polypeptides and antibodies against the
CC polypeptides may be used to determine the expression level of a tumour
CC protein of the invention, and therefore to determine whether cancer cells
CC are present. Such diagnostic methods may also be used to monitor the
CC progression of a cancer by repeating the processes at time intervals, and
CC comparing the current result to previous results. The present sequence
CC represents a cDNA encoding a human colon tumour polypeptide
XX
SQ Sequence 508 BP; 153 A; 89 C; 103 G; 163 T; 0 U; 0 Other;

Query Match 61.6%; Score 499; DB 3; Length 508;
Best Local Similarity 100.0%; Pred. No. 9.4e-140;
Matches 499; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 312 CGAGGAGTCGCTTAAGTGCAGGACCTCAAAGTGGGACAATATTTGTAAAGATCCAAA 371
Db 1 CGAGGAGTCGCTTAAGTGCAGGACCTCAAAGTGGGACAATATTTGTAAAGATCCAAA 60

Qy 372 AATAAATGACGCTACGCAAGAACCAACTGTACAAACTACACAGCTCATGTTCTG 431
Db 61 AATAAATGACGCTACGCAAGAACCAACTGTACAAACTACACAGCTCATGTTCTG 120

Qy 432 TTTTCCAGCACCCAACATAACTTGTAAGGATTCCAGTGGCAATGAAACACATTACTGG 491
Db 121 TTTTCCAGCACCCAACATAACTTGTAAGGATTCCAGTGGCAATGAAACACATTACTGG 180

Qy	492	GAACGAAGTTGGTTTTCAAGCCCATATCTGCCGAAATGTAAATGGCTATTCTACAA	551
Db	181	GAACGAAGTTGGTTTTCAAGCCCATATCTGCCGAAATGTAAATGGCTATTCTACAA	240
Qy	552	AGTGGCAGTCGCATTGCTCTTTCTGGATGGTGGAGCAGATCGATTTACCTGG	611
Db	241	AGTGGCAGTCGCATTGCTCTTTCTGGATGGTGGAGCAGATCGATTTACCTGG	300
Qy	612	ATACCCTGCTTGTTGGTTGTTAAAGTTTGCAGTGTAGGGTTTGGAATTGGAGCCT	671
Db	301	ATACCCTGCTTGTTGGTTGTTAAAGTTTGCAGTGTAGGGTTTGGAATTGGAGCCT	360
Qy	672	AATTGATTCATTCTATTCAATGCAGATTGTTGGACCTTCAGATGGAAGTAGTTACAT	731
Db	361	AATTGATTCATTCTATTCAATGCAGATTGTTGGACCTTCAGATGGAAGTAGTTACAT	420
Qy	732	TATAGATTACTATGGAACCAGACTACAAGACTGAGTATTACTAATGAAACATTTAGAAA	791
Db	421	TATAGATTACTATGGAACCAGACTACAAGACTGAGTATTACTAATGAAACATTTAGAAA	480
Qy	792	AACGCAATTATATCCATAA	810
Db	481	AACGCAATTATATCCATAA	499

RESULT 8

AAI28684

ID AAI28684 standard; cDNA; 508 BP.

XX

AC AAI28684;

XX

DT 12-OCT-2001 (first entry)

XX

DE Colon tumour related determined cDNA sequence for clone 25275.

XX

KW Human; immunotherapy; diagnosis; colon cancer; colon tumour; immunogenic;
KW gene therapy; vaccine; colonic cancer; ss.

XX

OS Homo sapiens.

XX

PN WO200149716-A2.

XX

PD 12-JUL-2001.

XX

PF 29-DEC-2000; 2000WO-US035596.

XX

PR 30-DEC-1999; 99US-00476296.

PR 10-JAN-2000; 2000US-00480321.

PR 15-FEB-2000; 2000US-00504629.

PR 06-MAR-2000; 2000US-00519444.

PR 19-MAY-2000; 2000US-00575251.

PR 29-JUN-2000; 2000US-00609448.

PR 28-AUG-2000; 2000US-00649811.

XX

PA (CORI-) CORIXA CORP.

XX

PI Xu J, Lodes MJ, Secrist H, Benson DR, Meagher MJ, Stolk JA;

PI King GE, Wang T, Jiang Y;

XX

DR WPI; 2001-441847/47.

XX

PT Colon tumor associated proteins and nucleic acids useful for the prevention, diagnosis and treatment of colonic cancer.

XX

PS Claim 2; Page 198; 472pp; English.

XX

CC The present invention describes colon tumour associated proteins (I) and
CC the polynucleotides (II) that encode them. (I) have cytostatic activity.
CC (I) and (II) can be used in gene therapy and vaccine production. (I) and
CC (II) may be used in the prevention, diagnosis and treatment of diseases
CC associated with inappropriate colon tumour associated protein (TCAP)
CC expression, such as colonic cancer. For example, (I) and (II) may be used
CC to treat disorders associated with decreased expression by rectifying
CC mutations or deletions in a patient's genome that affect the activity of
CC TCAPs by expressing inactive proteins or to supplement the patients own
CC production of them. Additionally, (II) may be used to produce the TCAP
CC proteins, by inserting the nucleic acids into a host cell culturing the
CC cell to express the protein. (II) and its complementary sequences may
CC also be used as DNA probes in diagnostic polymerase chain reaction (PCR)
CC and hybridisation assays to detect and quantitate the presence of similar
CC nucleic acids in samples, and therefore which patients may be in need of
CC restorative therapy. (I) may also be used as antigens in the production
CC of antibodies against TCAPs and in assays to identify modulators of TCAP
CC expression and activity. Anti-(I) antibodies and antagonists may also be
CC used to down regulate TCAP expression and activity. The anti-(I)
CC antibodies may also be used as diagnostic agents for detecting the
CC presence of TCAPs in samples (e.g. by enzyme linked immunosorbant assay
CC (ELISA)). AAI28460 to AAI29512 and AAM24494 to AAM24523 represent
CC nucleotide and amino acid sequences given in the exemplification of the
CC present invention

XX

SQ Sequence 508 BP; 153 A; 89 C; 103 G; 163 T; 0 U; 0 Other;

Query Match 61.6%; Score 499; DB 4; Length 508;
Best Local Similarity 100.0%; Pred. No. 9.4e-140;
Matches 499; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 312 CGAGGAGTCGCTTAAGTGCAGGACCTCAAAGTGGACAATATATTGTAAAGATCCAAA 371
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 1 CGAGGAGTCGCTTAAGTGCAGGACCTCAAAGTGGACAATATATTGTAAAGATCCAAA 60

Qy 372 AATAAATGACGCTACGCAAGAACCAAGTTAACTGTACAAACTACACAGCTCATGTTCTG 431
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 61 AATAAATGACGCTACGCAAGAACCAAGTTAACTGTACAAACTACACAGCTCATGTTCTG 120

Qy 432 TTTTCCAGCACCCAACATAACTTGTAAAGGATTCCAGTGGCAATGAAACACATTACTGG 491
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 121 TTTTCCAGCACCCAACATAACTTGTAAAGGATTCCAGTGGCAATGAAACACATTACTGG 180

Qy 492 GAACGAAGTTGGTTTTCAAGCCCATATCTTGGCAATGAAATGGCTATTCCCTACAA 551
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 181 GAACGAAGTTGGTTTTCAAGCCCATATCTTGGCAATGAAATGGCTATTCCCTACAA 240

Qy 552 AGTGGCAGTCGCATTGTCTCTTCTGGATGGTGGAGCAGATCGATTACCTTGG 611

Db ||||||| 241 AGTGGCAGTCGCATTGCTCTTTCTTGGATGGTGGAGCAGATCGATTACCTGG 300
Qy 612 ATACCCTGCTTGTTAAAGTTGCAGTGTAGGGTTGTGAATTGGGAGCCT 671
Db ||||||| 301 ATACCCTGCTTGTTAAAGTTGCAGTGTAGGGTTGTGAATTGGGAGCCT 360
Qy 672 AATTGATTCATTCTTCAATGCAGATTGGACCTTCAGATGGAAGTAGTTACAT 731
Db ||||||| 361 AATTGATTCATTCTTCAATGCAGATTGGACCTTCAGATGGAAGTAGTTACAT 420
Qy 732 TATAGATTACTATGAAACCAGACTTACAAGACTGAGTATTACTAATGAAACATTAGAAA 791
Db ||||||| 421 TATAGATTACTATGAAACCAGACTTACAAGACTGAGTATTACTAATGAAACATTAGAAA 480
Qy 792 AACGCAATTATATCCATAA 810
Db ||||||| 481 AACGCAATTATATCCATAA 499

RESULT 9

AAI28696

ID AAI28696 standard; cDNA; 508 BP.

XX

AC AAI28696;

XX

DT 12-OCT-2001 (first entry)

XX

DE Colon tumour related determined cDNA sequence for clone 25288.

XX

KW Human; immunotherapy; diagnosis; colon cancer; colon tumour; immunogenic;
KW gene therapy; vaccine; colonic cancer; ss.

XX

OS Homo sapiens.

XX

PN WO200149716-A2.

XX

PD 12-JUL-2001.

XX

PF 29-DEC-2000; 2000WO-US035596.

XX

PR 30-DEC-1999; 99US-00476296.

PR 10-JAN-2000; 2000US-00480321.

PR 15-FEB-2000; 2000US-00504629.

PR 06-MAR-2000; 2000US-00519444.

PR 19-MAY-2000; 2000US-00575251.

PR 29-JUN-2000; 2000US-00609448.

PR 28-AUG-2000; 2000US-00649811.

XX

PA (CORI-) CORIXA CORP.

XX

PI Xu J, Lodes MJ, Secrist H, Benson DR, Meagher MJ, Stolk JA;

PI King GE, Wang T, Jiang Y;

XX

DR WPI; 2001-441847/47.

XX

PT Colon tumor associated proteins and nucleic acids useful for the

PT prevention, diagnosis and treatment of colonic cancer.

XX

PS Claim 2; Page 201; 472pp; English.

XX

CC The present invention describes colon tumour associated proteins (I) and
CC the polynucleotides (II) that encode them. (I) have cytostatic activity.
CC (I) and (II) can be used in gene therapy and vaccine production. (I) and
CC (II) may be used in the prevention, diagnosis and treatment of diseases
CC associated with inappropriate colon tumour associated protein (TCAP)
CC expression, such as colonic cancer. For example, (I) and (II) may be used
CC to treat disorders associated with decreased expression by rectifying
CC mutations or deletions in a patient's genome that affect the activity of
CC TCAPs by expressing inactive proteins or to supplement the patients own
CC production of them. Additionally, (II) may be used to produce the TCAP
CC proteins, by inserting the nucleic acids into a host cell culturing the
CC cell to express the protein. (II) and its complementary sequences may
CC also be used as DNA probes in diagnostic polymerase chain reaction (PCR)
CC and hybridisation assays to detect and quantitate the presence of similar
CC nucleic acids in samples, and therefore which patients may be in need of
CC restorative therapy. (I) may also be used as antigens in the production
CC of antibodies against TCAPs and in assays to identify modulators of TCAP
CC expression and activity. Anti-(I) antibodies and antagonists may also be
CC used to down regulate TCAP expression and activity. The anti-(I)
CC antibodies may also be used as diagnostic agents for detecting the
CC presence of TCAPs in samples (e.g. by enzyme linked immunosorbant assay
CC (ELISA)). AAI28460 to AAI29512 and AAM24494 to AAM24523 represent
CC nucleotide and amino acid sequences given in the exemplification of the
CC present invention

XX

SQ Sequence 508 BP; 153 A; 89 C; 103 G; 163 T; 0 U; 0 Other;

Query Match 61.68; Score 499; DB 4; Length 508;
Best Local Similarity 100.0%; Pred. No. 9.4e-140;
Matches 499; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 312 CGAGGAGTCGCTTAAGTGCAGGGACCTCAAAGTGGGACAATATATTGTAAAGATCCAAA 371
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 CGAGGAGTCGCTTAAGTGCAGGGACCTCAAAGTGGGACAATATATTGTAAAGATCCAAA 60

Qy 372 AATAATGACGCTACGCAAGAACCAAGTTAACGTACAAACTACACAGCTCATGTTCTG 431
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 61 AATAATGACGCTACGCAAGAACCAAGTTAACGTACAAACTACACAGCTCATGTTCTG 120

Qy 432 TTTCCAGCACCAACATAACTTGTAAAGGATCCAGTGGCAATGAAACACATTACTGG 491
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 121 TTTCCAGCACCAACATAACTTGTAAAGGATCCAGTGGCAATGAAACACATTACTGG 180

Qy 492 GAACGAAGTTGGTTTTCAAGCCCATACTGCCGAAATGTAAATGGCTATTCTACAA 551
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 181 GAACGAAGTTGGTTTTCAAGCCCATACTGCCGAAATGTAAATGGCTATTCTACAA 240

Qy 552 AGTGGCAGTCGCATTGTCTCTTTCTGGATGGTGGGAGCAGATCGATTACCTGG 611
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 241 AGTGGCAGTCGCATTGTCTCTTTCTGGATGGTGGGAGCAGATCGATTACCTGG 300

Qy 612 ATACCCTGCTTGGTTGTTAAAGTTGCACTGTAGGGTTTGGAATTGGAGCCT 671
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 301 ATACCCTGCTTGGGTTGTTAAAGTTGCAGACTGTAGGGTTGTGGAATTGGGAGCCT 360
Qy 672 AATTGATTCATTCTTATTCAATGCAGATTGTTGGACCTTCAGATGGAAGTAGTTACAT 731
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 361 AATTGATTCATTCTTATTCAATGCAGATTGTTGGACCTTCAGATGGAAGTAGTTACAT 420
Qy 732 TATAGATTACTATGGAACCAGACTACAAGACTGAGTATTACTAATGAAACATTTAGAAA 791
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 421 TATAGATTACTATGGAACCAGACTACAAGACTGAGTATTACTAATGAAACATTTAGAAA 480
Qy 792 AACGCAATTATATCCATAA 810
||| ||| ||| ||| |||
Db 481 AACGCAATTATATCCATAA 499

RESULT 10
ABZ32882
ID ABZ32882 standard; cDNA; 508 BP.
XX
AC ABZ32882;
XX
DT 30-JAN-2003 (first entry)
XX
DE Human colon tumour cDNA clone 25288 SEQ ID NO:245.
XX
KW Human; colon cancer; colon tumour; immunotherapy; diagnosis; cancer;
KW tumour; immune response; immunostimulant; cytostatic; vaccine; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200283070-A2.
XX
PD 24-OCT-2002.
XX
PF 09-APR-2002; 2002WO-US011475.
XX
PR 10-APR-2001; 2001US-00833263.
PR 03-AUG-2001; 2001US-00922217.
PR 19-DEC-2001; 2001US-00025380.
XX
PA (CORI-) CORIXA CORP.
XX
PI Xu J, Lodes MJ, Secrist H, Benson DR, Meagher MJ, Stolk JA;
PI Wang T, Jiang Y, Smith CL, King GE, Wang A, Clapper JD, Skeiky YAW;
PI Fanger GR, Vedvick TS, Carter D;
XX
DR WPI; 2003-067548/06.
XX
PT New polynucleotide, useful for the preparation of a composition for
PT stimulating an immune response against, or treating, cancer.
XX
PS Example 1; Page 204; 537pp; English.
XX
CC The present invention describes compounds (I) for the immunotherapy and
CC diagnosis of colon cancer. Also described: (1) a method for detecting the
CC presence of cancer in a patient; (2) a method for stimulating and/or
CC expanding T cells specific for a tumour protein; (3) an isolated T cell

CC population comprising T cells prepared by the method of (2); (4) a method
CC for stimulating an immune response in a patient; (5) a method for
CC treating cancer in a patient; and (6) a method for inhibiting the
CC development of cancer in a patient. (I) have immunostimulant and
CC cytostatic activities and can be used in vaccines. ABZ32646 to ABZ33725
CC and ABP55343 to ABP55391 represent human colon cancer/tumour related
CC sequences used in the exemplification of the present invention
XX

SQ Sequence 508 BP; 153 A; 89 C; 103 G; 163 T; 0 U; 0 Other;

Query Match 61.6%; Score 499; DB 7; Length 508;
Best Local Similarity 100.0%; Pred. No. 9.4e-140;
Matches 499; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	312 CGAGGAGTCGCTTAAGTGCAGGACCTCAAAGTGGGACAATATATTGTAAAGATCCAAA	371
Db	1 CGAGGAGTCGCTTAAGTGCAGGACCTCAAAGTGGGACAATATATTGTAAAGATCCAAA	60
Qy	372 AATAAATGACGCTACGCAAGAACCAAGCTTAACGTACAAACTACACAGCTCATGTTCTG	431
Db	61 AATAAATGACGCTACGCAAGAACCAAGCTTAACGTACAAACTACACAGCTCATGTTCTG	120
Qy	432 TTTTCCAGCACCCAACATAACTTGTAAAGGATTCCAGTGGCAATGAAACACATTACTGG	491
Db	121 TTTTCCAGCACCCAACATAACTTGTAAAGGATTCCAGTGGCAATGAAACACATTACTGG	180
Qy	492 GAACGAAGTTGGTTTTCAAGCCCATATCTTGCAGCGAAATGTAAATGGCTATTCTACAA	551
Db	181 GAACGAAGTTGGTTTTCAAGCCCATATCTTGCAGCGAAATGTAAATGGCTATTCTACAA	240
Qy	552 AGTGGCAGTCGATTGTCCTTTCTGGATGGTGGAGCAGATCGATTACCTTGG	611
Db	241 AGTGGCAGTCGATTGTCCTTTCTGGATGGTGGAGCAGATCGATTACCTTGG	300
Qy	612 ATACCCTGCTTGTTGGTTGTAAAGTTTGCAGTGTAGGGTTTGTGGAATTGGGAGCCT	671
Db	301 ATACCCTGCTTGTTGGTTGTAAAGTTTGCAGTGTAGGGTTTGTGGAATTGGGAGCCT	360
Qy	672 AATTGATTCATTCTATTCAATGCAGATTGTTGGACCTTCAGATGGAAGTAGTTACAT	731
Db	361 AATTGATTCATTCTATTCAATGCAGATTGTTGGACCTTCAGATGGAAGTAGTTACAT	420
Qy	732 TATAGATTACTATGGAACCAGACTTACAAGACTGAGTATTACTAATGAAACATTTAGAAA	791
Db	421 TATAGATTACTATGGAACCAGACTTACAAGACTGAGTATTACTAATGAAACATTTAGAAA	480
Qy	792 AACGCAATTATATCCATAA	810
Db	481 AACGCAATTATATCCATAA	499

RESULT 11

ABZ32870

ID ABZ32870 standard; cDNA; 508 BP.

XX

AC ABZ32870;

XX

DT 30-JAN-2003 (first entry)
XX
DE Human colon tumour cDNA clone 25275 SEQ ID NO:233.
XX
KW Human; colon cancer; colon tumour; immunotherapy; diagnosis; cancer;
KW tumour; immune response; immunostimulant; cytostatic; vaccine; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200283070-A2.
XX
PD 24-OCT-2002.
XX
PF 09-APR-2002; 2002WO-US011475.
XX
PR 10-APR-2001; 2001US-00833263.
PR 03-AUG-2001; 2001US-00922217.
PR 19-DEC-2001; 2001US-00025380.
XX
PA (CORI-) CORIXA CORP.
XX
PI Xu J, Lodes MJ, Secrist H, Benson DR, Meagher MJ, Stolk JA;
PI Wang T, Jiang Y, Smith CL, King GE, Wang A, Clapper JD, Skeiky YAW;
PI Fanger GR, Vedvick TS, Carter D;
XX
DR WPI; 2003-067548/06.
XX
PT New polynucleotide, useful for the preparation of a composition for
PT stimulating an immune response against, or treating, cancer.
XX
PS Example 1; Page 201; 537pp; English.
XX
CC The present invention describes compounds (I) for the immunotherapy and
CC diagnosis of colon cancer. Also described: (1) a method for detecting the
CC presence of cancer in a patient; (2) a method for stimulating and/or
CC expanding T cells specific for a tumour protein; (3) an isolated T cell
CC population comprising T cells prepared by the method of (2); (4) a method
CC for stimulating an immune response in a patient; (5) a method for
CC treating cancer in a patient; and (6) a method for inhibiting the
CC development of cancer in a patient. (I) have immunostimulant and
CC cytostatic activities and can be used in vaccines. ABZ32646 to ABZ33725
CC and ABP55343 to ABP55391 represent human colon cancer/tumour related
CC sequences used in the exemplification of the present invention
XX
SQ Sequence 508 BP; 153 A; 89 C; 103 G; 163 T; 0 U; 0 Other;

Query Match 61.6%; Score 499; DB 7; Length 508;
Best Local Similarity 100.0%; Pred. No. 9.4e-140;
Matches 499; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 312 CGAGGAGTCGCTTAAGTGCAGGACCTCAAAGTGGACAATATTTGTAAAGATCCAAA 371
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 CGAGGAGTCGCTTAAGTGCAGGACCTCAAAGTGGACAATATTTGTAAAGATCCAAA 60

Qy 372 ATAATGACGCTACGCAAGAACCGAGTTAACTGTACAAACTACACAGCTCATGTTCTG 431
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 61 ATAATGACGCTACGCAAGAACCGAGTTAACTGTACAAACTACACAGCTCATGTTCTG 120

Qy	432 TTTTCCAGCACCAACATAACTTGTAAAGGATTCAGTGGCAATGAAACACATTACTGG	491
Db	121 TTTTCCAGCACCAACATAACTTGTAAAGGATTCAGTGGCAATGAAACACATTACTGG	180
Qy	492 GAACGAAGTTGGTTTTCAAGCCATATCTGCCGAAATGTAAATGGCTATTCTACAA	551
Db	181 GAACGAAGTTGGTTTTCAAGCCATATCTGCCGAAATGTAAATGGCTATTCTACAA	240
Qy	552 AGTGGCAGTCGCATTGTCTCTTTCTTGGATGGTGGAGCAGATCGATTACCTGG	611
Db	241 AGTGGCAGTCGCATTGTCTCTTTCTTGGATGGTGGAGCAGATCGATTACCTGG	300
Qy	612 ATACCCTGCTTGTTGGTTAAAGTTGCAGTTGGATGGGAGCCT 671	
Db	301 ATACCCTGCTTGTTGGTTAAAGTTGCAGTTGGATGGGAGCCT 360	
Qy	672 AATTGATTCATTCTATTCAATGCAGATTGGACCTTCAGATGGAAGTAGTTACAT	731
Db	361 AATTGATTCATTCTATTCAATGCAGATTGGACCTTCAGATGGAAGTAGTTACAT	420
Qy	732 TATAGATTACTATGGAACCAGACTTACAAGACTGAGTATTACTAATGAAACATTAGAAA	791
Db	421 TATAGATTACTATGGAACCAGACTTACAAGACTGAGTATTACTAATGAAACATTAGAAA	480
Qy	792 AACGCAATTATATCCATAA 810	
Db	481 AACGCAATTATATCCATAA 499	

RESULT 12

ABK52558

ID ABK52558 standard; cDNA; 1095 BP.

XX

AC ABK52558;

XX

DT 13-AUG-2002 (first entry)

XX

DE cDNA encoding RNA polymerase II subunit 11.

XX

KW RNA polymerase II subunit 11; ss; gene; cancer; HIV; infection;

KW human immunodeficiency virus.

XX

OS Unidentified.

XX

FH Key Location/Qualifiers

FT CDS 12..314

FT /*tag= a

FT /product= "RNA polymerase II subunit 11"

XX

PN CN1331300-A.

XX

PD 16-JAN-2002.

XX

PF 30-JUN-2000; 2000CN-00116963.

XX

PR 30-JUN-2000; 2000CN-00116963.

XX
PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.
XX
PI Mao Y, Xie Y;
XX
DR WPI; 2002-340664/38.
DR P-PSDB; AAU97631.
XX
PT Polypeptide-RNA polymerase II subunit 11 and polynucleotide for coding
PT it.
XX
PS Claim 6; Page 28-29; 32pp; Chinese.
XX
CC This invention relates to the DNA and protein sequences of a novel
CC polypeptide-RNA polymerase II subunit 11 protein. The invention also
CC comprises a process for preparing the polypeptide of the invention by DNA
CC recombination, the application of the polypeptide in treating diseases
CC such as cancer, human immunodeficiency virus (HIV) infection, etc, the
CC antagonist of the polypeptide and its medical action, and the application
CC of the said polynucleotide are disclosed. The present sequence represents
CC the cDNA sequence encoding the RNA polymerase II subunit 11 protein of
CC the invention
XX
SQ Sequence 1095 BP; 268 A; 230 C; 244 G; 353 T; 0 U; 0 Other;

Query Match 54.6%; Score 442.2; DB 6; Length 1095;
Best Local Similarity 81.1%; Pred. No. 1.9e-122;
Matches 596; Conservative 0; Mismatches 38; Indels 101; Gaps 3;

Qy 177 GGTCTCCAAGATGGCGGCCGCCTGGCGTCTGGTCCGCTGCTCCGGAGGCCGTGACGGC 236
Db 2 GGTCTCCAAGATGGCGGCCGCCTGGCGTCTGGTCCGCTGCTCCGGATGCCGTGACGGC 61

Qy 237 CAGACTCGTTGGTGTCCCTGTGGTCGTCTCAGTCACTACAGGACCTGGGGGGCTGTTGC 296
Db 62 CAGACTCGTTGGTGTCCCTGTGGTCGTCTCAGTCACTACAGGACCTGGGGGGCTGTTGC 121

Qy 297 CACCTCCGCCGGGGCGAGGAGTCGCTTAAGTGCAGGACCTCAAAGTGGGACAATAT-A 355
Db 122 CACCTCCGCCGGGGCGAGGAGTCGCTTAAGTGCAGGACCTCAAAGTGGGACAATATCC 181

Qy 356 TTTGTAAAGATCCAAAATAATGACGCTA-----CGCAAGAACCAAGTTAA 401
Db 182 TCTGTGGAGAACACCCCCCATGGAGGCGAGGGTCTTACTCTGTGCCCTGGCTGGAGTA 241

Qy 402 CTGTACAAACTACACAGCTCA----- 422
Db 242 CAGTGGCACGATCTCAGCTCACTGCAGCCTCCGCCCTGGGTTCAAGTCATTCTCCTGC 301

Qy 423 -----TGTTTCTGTTT 435
Db 302 CTCAGCCTCCTGAGTAGCTGGACTACAGGCATGCGCCACCACACCCGGTTCTGTTT 361

Qy 436 CCAGCACCCAACATAACTTGTAAAGGATTCCAGTGGCAATGAAACACATTACTGGGAAC 495
Db 362 CCAGCACCCAACATAACTTGTAAAGGATTCCAGTGGCAATGAAACACATTACTGGGAAC 421

Qy 496 GAAGTTGGTTTTCAAGCCCATACTGCCGAAATGTAAATGGCTATTCCCTACAAAGTG 555
|||
Db 422 GAAGTTGGTTTTCAAGCCCATACTGCCGAAATGTAAATGGCTATTCCCTACAAAGTG 481

Qy 556 GCAGTCGCATTGTCTCTTCTGGATGGTGGAGCAGATCGATTTACCTGGATAC 615
|||
Db 482 GCAGTCGCATTGTCTCTTCTGGATGGTGGAGCAGATCGATTTACCTGGATAC 541

Qy 616 CCTGCTTGTTGGTTGTAAAGTTGCACTGTAGGGTTGTGGAATTGGGAGCCTAATT 675
|||
Db 542 CCTGCTTGTTGGTTGTAAAGTTGCACTGTAGGGTTGTGGAATTGGGAGCCTAATT 601

Qy 676 GATTCATTCTTATTCAATGCAGATTGGACCTTCAGATGGAAGTAGTTACATTATA 735
|||
Db 602 GATTCATTCTTATTCAATGCAGATTGGACCTTCAGATGGAAGTAGTTACATTATA 661

Qy 736 GATTACTATGGAACCAGACTTACAAGACTGAGTATTACTAATGAAACATTTAGAAAAACG 795
|||
Db 662 GATTACTATGGAACCAGACTTACAAGACTGAGTATTACTAATGAAACATTTAGAAAAACG 721

Qy 796 CAATTATATCCATAA 810
|||
Db 722 CAATTATATCCATAA 736

RESULT 13

AAX41191

ID AAX41191 standard; cDNA; 440 BP.

XX

AC AAX41191;

XX

DT 17-JUN-1999 (first entry)

XX

DE Human secreted protein 5' EST SEQ ID NO:135.

XX

KW Human; secreted protein; EST; expressed sequence tag; diagnosis;
KW forensic; gene therapy; chromosome mapping; signal peptide;
KW upstream regulatory sequence; cytokine activity; cell proliferation;
KW differentiation; haematopoiesis regulation; tissue growth regulation;
KW reproductive hormone regulation; chemotactic; chemokinetic; haemostatic;
KW thrombolytic; anti-inflammatory; tumour inhibition; ds.

XX

OS Homo sapiens.

XX

PN WO9906548-A2.

XX

PD 11-FEB-1999.

XX

PF 31-JUL-1998; 98WO-IB001222.

XX

PR 01-AUG-1997; 97US-00905135.

XX

PA (GEST) GENSET.

XX

PI Dumas Milne Edwards J, Duclert A, Lacroix B;

XX

DR WPI; 1999-153778/13.

XX

DR P-PSDB; AAY12358.

XX

PT New nucleic acids encoding human secreted proteins - obtained from cDNA
PT libraries prepared from e.g. liver, ovary, brain, prostate, kidney, lung,
PT umbilical cord, placenta and colon tissue.

XX

PS Claim 1; Page 315; 824pp; English.

XX

CC AAX41094 to AAX41347 represent 5' expressed sequence tags (ESTs) for
CC human secreted proteins, and encode the proteins given in AAY12261 to
CC AAY12514, respectively. The proteins given represent the signal peptide
CC and an N-terminal fragment of a secreted protein. The nucleic acid
CC sequences can be used for producing secreted human gene products. They
CC can also be used to develop products for diagnosis and therapy. The
CC proteins obtained may have cytokine activity, cell
CC proliferation/differentiation activity, haematopoiesis regulating
CC activity, tissue growth regulating activity, reproductive hormone
CC regulating activity, chemotactic/ chemokinetic activity, haemostatic and
CC thrombolytic activity, receptor/ ligand activity, anti-inflammatory
CC activity, tumour inhibition activity or other activities. The products
CC can be used in forensic, gene therapy and chromosome mapping procedures.
CC The sequences can also be used for obtaining corresponding promoter
CC sequences. The nucleic acids encoding the signal peptide can be used for
CC directing extracellular secretion of a polypeptide or the insertion of a
CC polypeptide into a membrane, or importing a polypeptide into a cell

XX

SQ Sequence 440 BP; 107 A; 103 C; 114 G; 114 T; 0 U; 2 Other;

Query Match 53.9%; Score 436.8; DB 2; Length 440;
Best Local Similarity 99.5%; Pred. No. 4.9e-121;
Matches 436; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 166 GAGAAAGTGTGGTCTCCAAGATGGCGGCCGCCTGGCGTCTGGTCCGTCTGCTCCGGAG 225
||| ||| ||| ||| ||| ||| ||| :||| ||| ||| ||| ||| |||

Db 3 GAGAAAGTGTGGTCTCCAAGATGGCGGCCGCCTGGCSDTCTGGTCCGTCTGCTCCGGAG 62

Qy 226 GCCGTGACGCCAGACTCGTTGGTGCCTGTGGTCGCTCAGTCAGTCACTACAGGACCTGG 285
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 63 GCCGTGACGCCAGACTCGTTGGTGCCTGTGGTCGCTCAGTCAGTCACTACAGGACCTGG 122

Qy 286 GGGGCTGTTGCCACCTCCGCCGGGGCGAGGAGTCGCTTAAGTGCAGGACCTCAAAGTG 345
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 123 GGGGCTGTTGCCACCTCCGCCGGGGCGAGGAGTCGCTTAAGTGCAGGACCTCAAAGTG 182

Qy 346 GGACAATATATTGTAAAGATCCAAAATAATGACGCTACGCAAGAACCGAGTTAAGTGT 405
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 183 GGACAATATATTGTAAAGATCCAAAATAATGACGCTACGCAAGAACCGAGTTAAGTGT 242

Qy 406 ACAAAACTACACAGCTCATGTTCCGTGTTCCAGCACCCAACATAACTTGTAAAGGATTCC 465
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 243 ACAAAACTACACAGCTCATGTTCCGTGTTCCAGCACCCAACATAACTTGTAAAGGATTCC 302

Qy 466 AGTGGCAATGAAACACATTACTGGAACGAAGTTGGTTTTCAAGCCCATATCTTGC 525
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 303 AGTGGCAATGAAACACATTACTGGAACGAAGTTGGTTTTCAAGCCCATATCTTGC 362

Qy 526 CGAAATGTAAATGGCTATTCCCTACAAAGTGGCAGTCGCATTGTCTTTCTGGATGG 585

Db ||||||| 363 CGAAATGTAAATGGCTATTCCCTACAAAGTGGCAGTCGCATTGTCTTTTCTGGATGG 422
Qy ||||| 586 TTGGGAGCAGATCGATT 603
Db ||||| 423 TTGGGAGCAGATCGATT 440

RESULT 14

AAX41259

ID AAX41259 standard; cDNA; 455 BP.

XX

AC AAX41259;

XX

DT 17-JUN-1999 (first entry)

XX

DE Human secreted protein 5' EST SEQ ID NO:203.

XX

KW Human; secreted protein; EST; expressed sequence tag; diagnosis;
KW forensic; gene therapy; chromosome mapping; signal peptide;
KW upstream regulatory sequence; cytokine activity; cell proliferation;
KW differentiation; haematopoiesis regulation; tissue growth regulation;
KW reproductive hormone regulation; chemotactic; chemokinetic; haemostatic;
KW thrombolytic; anti-inflammatory; tumour inhibition; ds.

XX

OS Homo sapiens.

XX

PN WO9906548-A2.

XX

PD 11-FEB-1999.

XX

PF 31-JUL-1998; 98WO-IB001222.

XX

PR 01-AUG-1997; 97US-00905135.

XX

PA (GEST) GENSET.

XX

PI Dumas Milne Edwards J, Duclert A, Lacroix B;

XX

DR WPI; 1999-153778/13.

DR P-PSDB; AAY12426.

XX

PT New nucleic acids encoding human secreted proteins - obtained from cDNA
PT libraries prepared from e.g. liver, ovary, brain, prostate, kidney, lung,
PT umbilical cord, placenta and colon tissue.

XX

PS Claim 1; Page 456; 824pp; English.

XX

CC AAX41094 to AAX41347 represent 5' expressed sequence tags (ESTs) for
CC human secreted proteins, and encode the proteins given in AAY12261 to
CC AAY12514, respectively. The proteins given represent the signal peptide
CC and an N-terminal fragment of a secreted protein. The nucleic acid
CC sequences can be used for producing secreted human gene products. They
CC can also be used to develop products for diagnosis and therapy. The
CC proteins obtained may have cytokine activity, cell
CC proliferation/differentiation activity, haematopoiesis regulating
CC activity, tissue growth regulating activity, reproductive hormone

CC regulating activity, chemotactic/ chemokinetic activity, haemostatic and
CC thrombolytic activity, receptor/ ligand activity, anti-inflammatory
CC activity, tumour inhibition activity or other activities. The products
CC can be used in forensic, gene therapy and chromosome mapping procedures.
CC The sequences can also be used for obtaining corresponding promoter
CC sequences. The nucleic acids encoding the signal peptide can be used for
CC directing extracellular secretion of a polypeptide or the insertion of a
CC polypeptide into a membrane, or importing a polypeptide into a cell

xx

SO Sequence 455 BP; 102 A; 107 C; 115 G; 122 T; 0 U; 9 Other;

Query Match 52.5%; Score 425.2; DB 2; Length 455;
Best Local Similarity 96.3%; Pred. No. 1.6e-117;
Matches 439; Conservative 3; Mismatches 12; Indels 2; Gaps 1;

Qy 177 GGTCTCCAAGATGGCGGCCGCTGGCCGTCTGGTCCGTCTGCTCCGGAGGCCGTGACGGC 236
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
S 61 GGTCTCCAAGATGGCGGCCGCTGGCCGTCTGGTCCGTCTGCTCCGGAGGCCGTGACGGC

Qy 297 CACCTCCGCCGGGGCGAGGAGTCGCTTAAGTGCAGGACCTCAAAGTGGGACAATATAT 356

Qy 357 TTGTAAAGATCCAAAATAATGACGCTACGCAAGAACCGAGTTAACTGTACAAACTACAC 416

Db 182 TTGTAAAGATCCAAAAATAAATGACGCTACGCAAGAACCGAGTTAACTGTACAAACTACAC 241
Qv 417 AGCTCATGTTCTGTTCAGCACCCAACATAACTTGTAAAGGATTCCAGTGGCAATGA 476

Db 242 AGCTCATGTTCTGTTCCAGCACCCAACATAACTGTAAGGATNCCAGTGGCAATGA 301

Db 302 AACACATTTACTGGGAACGAAGTTGGTTTTCAAGCCATATCTTGCCTGAAATGTAAA 361

Db 362 TGGCTATTCCTAC--NNTKAGCAGTNNNWTGTCTTTCTGGATGGTGGGAGCAGA 419

Qy	597 TCGATTTACCTTGATACCCTGCTTGGGTTGTT 632
Db	420 TCGATTTACCTTGATACCCTGCTTGGGTTGTT 455

RESULT 15

AAC04131

ID AAC04131 standard; cDNA; 487 BP.

xx

AC AAC04131;

xx

PT 06-OCT-2000 (first entry)

xx

DE Human secreted protein 5' EST, SEQ ID NO: 8206.

XX
KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
KW gene therapy; chromosome mapping; ss.
XX
OS Homo sapiens.
XX
PN EP1033401-A2.
XX
PD 06-SEP-2000.
XX
PF 21-FEB-2000; 2000EP-00200610.
XX
PR 26-FEB-1999; 99US-0122487P.
XX
PA (GEST) GENSET.
XX
PI Dumas Milne Edwards J, Duclert A, Giordano J;
XX
DR WPI; 2000-500381/45.
XX
PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for
PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
PT diagnostic, forensic, gene therapy and chromosome mapping procedures.
XX
PS Claim 1; SEQ ID NO 8206; 71pp + Sequence Listing; English.
XX
CC The present sequence is one of a large number of 5' ESTs derived from
CC mRNAs encoding secreted proteins. No ORF has yet been conclusively
CC identified within the present sequence. The 5' ESTs were prepared from
CC total human RNAs or polyA+ RNAs derived from 30 different tissues. EST
CC sequences usually correspond mainly to the 3' untranslated region (UTR)
CC of the mRNA because they are often obtained from oligo-dT primed cDNA
CC libraries. Such ESTs are not well suited for isolating cDNA sequences
CC derived from the 5' ends of mRNAs and even in those cases where longer
CC cDNA sequences have been obtained, the full 5' UTR is rarely included. 5'
CC ESTs are derived from mRNAs with intact 5' ends and can therefore be used
CC to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in
CC diagnostic, forensic, gene therapy and chromosome mapping procedures.
CC They are used to obtain upstream regulatory sequences and to design
CC expression and secretion vectors
XX
SQ Sequence 487 BP; 115 A; 118 C; 125 G; 120 T; 0 U; 9 Other;

Query Match 50.8%; Score 411.4; DB 3; Length 487;
Best Local Similarity 91.4%; Pred. No. 2.4e-113;
Matches 445; Conservative 9; Mismatches 10; Indels 23; Gaps 1;

Db 121 GGGGGGCTGTTGCCACCTCCGCCGGGGCRAGGAGTCGCTTAAGTGCAGGGACCTCAAAG 180
Qy 344 TGGGACAATATATT-----TGTAAAGATCCAAAATAATGA 380
||::||||||| |
Db 181 TGRRACAATATCCTCTGGAGAACACCCCCCATGGAGGCGAGATCCAAAATAATGA 240
Qy 381 CGCTACGCAAGAACCACTTAACGTACAAACTACACAGCTCATGTTCCCTGTTCCAGC 440
|||:|||||:|||||:|||||:
Db 241 CGCTACGCAAGAACCACTTAACGTACAAACTACACAGCTCATGTTCCCTGTTCCAGC 300
Qy 441 ACCCAACATAACTGTAAGGATTCCAGTGGCAATGAAACACATTTACTGGAACGAAGT 500
|||:|||||:|||||:|||||:
Db 301 ACCCAACATAACTGTAAGGATTCCAGTGGCAATGAAACACATTTACTGGAACGAAGT 360
Qy 501 TGGTTTTTCAAGCCCATATCTGCCGAAATGTAAATGGCTATTCCCTACAAAGTGGCAGT 560
|||:|||||:|||||:
Db 361 TGGTTTTTCAAGCCCATATCTGCCGAAATGTAAATGGCTATTCCCTACAAAGTGGCAGT 420
Qy 561 CGCATTGTCTCTTTCTTGGATGGTGGAGCAGATCGATTTACCTTGGATACCCTGC 620
|||:|||||:
Db 421 CGCATTGTCTCTTTCTTGGATGGTGGAGCAGATCGATTTACCTTGGATACCCTGC 480
Qy 621 TTTGGGT 627
|||:
Db 481 TTTGGGT 487

Search completed: March 4, 2004, 07:39:01

Job time : 390 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 4, 2004, 06:47:39 ; Search time 91 Seconds
(without alignments)
4939.673 Million cell updates/sec

Title: US-09-852-100B-1

Perfect score: 810

Sequence: 1 atgcatattttaaaagggtc.....aaacgcaattatatccataa 810

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result	Query					Description
No.	Score	Match	Length	DB	ID	
1	499	61.6	508	4	US-09-401-064-233	Sequence 233, App
2	499	61.6	508	4	US-09-401-064-245	Sequence 245, App
3	49.8	6.1	1455	3	US-09-276-531-33	Sequence 33, Appl
4	40.4	5.0	1119	4	US-09-489-039A-6022	Sequence 6022, Ap
5	38.6	4.8	392000	4	US-10-027-983-11	Sequence 11, Appl
6	36.8	4.5	4403765	3	US-09-103-840A-2	Sequence 2, Appl
7	36.4	4.5	1462	1	US-08-552-142A-16	Sequence 16, Appl
8	36.4	4.5	1951	1	US-08-910-973-16	Sequence 16, Appl
9	36.4	4.5	1951	4	US-09-499-227-16	Sequence 16, Appl
10	36.2	4.5	8093	4	US-10-204-708-32	Sequence 32, Appl
11	35.4	4.4	450	4	US-09-252-991A-12127	Sequence 12127, A

c	12	35.4	4.4	1404	4	US-09-252-991A-12291	Sequence 12291, A
	13	35.4	4.4	9347	4	US-10-204-708-36	Sequence 36, Appl
	14	35.4	4.4	580073	4	US-08-545-528D-1	Sequence 1, Appli
	15	35.2	4.3	4411529	3	US-09-103-840A-1	Sequence 1, Appli
c	16	35	4.3	1494	4	US-09-252-991A-7049	Sequence 7049, Ap
	17	35	4.3	4236	4	US-09-252-991A-7057	Sequence 7057, Ap
	18	35	4.3	7304	4	US-10-204-708-43	Sequence 43, Appl
c	19	35	4.3	10023	4	US-09-252-991A-6997	Sequence 6997, Ap
	20	35	4.3	1830121	4	US-09-557-884-1	Sequence 1, Appli
	21	35	4.3	1830121	4	US-09-643-990A-1	Sequence 1, Appli
	22	34.8	4.3	832	4	US-09-621-976-2813	Sequence 2813, Ap
c	23	34.6	4.3	4673	1	US-07-638-431-1	Sequence 1, Appli
c	24	34.6	4.3	4673	5	PCT-US92-00018-1	Sequence 1, Appli
	25	34	4.2	5152	4	US-10-204-708-47	Sequence 47, Appl
	26	34	4.2	11131	4	US-10-204-708-27	Sequence 27, Appl
	27	33.6	4.1	11049	4	US-10-204-708-23	Sequence 23, Appl
c	28	33.4	4.1	549	4	US-09-252-991A-14907	Sequence 14907, A
	29	33.4	4.1	1125	4	US-09-252-991A-14723	Sequence 14723, A
	30	33.4	4.1	1636	6	5447867-2	Patent No. 5447867
c	31	33.4	4.1	1854	4	US-09-252-991A-15029	Sequence 15029, A
	32	33.4	4.1	9179	4	US-08-956-171E-100	Sequence 100, App
c	33	33.4	4.1	319608	4	US-09-539-333D-1	Sequence 1, Appli
c	34	33.4	4.1	319608	4	US-09-679-409-1	Sequence 1, Appli
c	35	33	4.1	364	4	US-09-621-976-17202	Sequence 17202, A
c	36	33	4.1	3255	4	US-09-601-198-108	Sequence 108, App
	37	33	4.1	4029	4	US-09-620-312D-201	Sequence 201, App
	38	33	4.1	5152	4	US-10-204-708-48	Sequence 48, Appl
c	39	33	4.1	55298	4	US-09-491-356C-1	Sequence 1, Appli
c	40	32.8	4.0	988	1	US-08-243-545-5	Sequence 5, Appli
c	41	32.8	4.0	988	2	US-08-993-962-5	Sequence 5, Appli
c	42	32.8	4.0	988	3	US-09-160-841-5	Sequence 5, Appli
c	43	32.8	4.0	988	3	US-09-109-100-2	Sequence 2, Appli
c	44	32.8	4.0	988	4	US-08-669-692-5	Sequence 5, Appli
c	45	32.8	4.0	988	4	US-08-444-626-5	Sequence 5, Appli

ALIGNMENTS

RESULT 1

US-09-401-064-233

```
; Sequence 233, Application US/09401064
; Patent No. 6623923
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Lodes, Michael J.
; APPLICANT: Secrist, Heather
; APPLICANT: Benson, Darin R.
; APPLICANT: Meagher, Madeline Joy
; APPLICANT: Stolk, John A.
; APPLICANT: Wang, Tongtong
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF COLON CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.471C2
; CURRENT APPLICATION NUMBER: US/09/401,064
; CURRENT FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 371
```

; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 233
; LENGTH: 508
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-401-064-233

RESULT 2

US-09-401-064-245

: Sequence 245, Application US/09401064

Patent No. 6623923

GENERAL INFORMATION:

GENERAL INFORMATION:

; APPLICANT: xu, Jiangchuan

; APPLICANT: Lodes, Michael J.
; APPLICANT: Sosnick, Heather

; APPLICANT: Secrist, Heather
; APPLICANT: Bangor, Parin B

; APPLICANT: Meagher, Madeline Joy
; APPLICANT: Stolk, John A.
; APPLICANT: Wang, Tongtong
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF COLON CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.471C2
; CURRENT APPLICATION NUMBER: US/09/401,064
; CURRENT FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 371
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 245
; LENGTH: 508
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-401-064-245

Query Match 61.6%; Score 499; DB 4; Length 508;
Best Local Similarity 100.0%; Pred. No. 2.1e-153;
Matches 499; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	312	CGAGGAGTCGCTTAAGTGCAGGGACCTCAAAGTGGGACAATATATTGTAAAGATCCAAA	371
Db	1	CGAGGAGTCGCTTAAGTGCAGGGACCTCAAAGTGGGACAATATATTGTAAAGATCCAAA	60
Qy	372	AATAAATGACGCTACGCAAGAACCAAGTTAACGTACAAACTACACAGCTCATGTTCTG	431
Db	61	AATAAATGACGCTACGCAAGAACCAAGTTAACGTACAAACTACACAGCTCATGTTCTG	120
Qy	432	TTTCCAGCACCCAACATAACTTGTAAAGGATTCCAGTGGCAATGAAACACATTACTGG	491
Db	121	TTTCCAGCACCCAACATAACTTGTAAAGGATTCCAGTGGCAATGAAACACATTACTGG	180
Qy	492	GAACGAAGTTGGTTTTCAAGCCCATACTTGTAAAGGATTCCAGTGGCAATGAAACACATTACTGG	551
Db	181	GAACGAAGTTGGTTTTCAAGCCCATACTTGTAAAGGATTCCAGTGGCAATGAAACACATTACTGG	240
Qy	552	AGTGGCAGTCGATTGTCTCTTTCTTGGATGGTGGAGCAGATCGATTACCTTGG	611
Db	241	AGTGGCAGTCGATTGTCTCTTTCTTGGATGGTGGAGCAGATCGATTACCTTGG	300
Qy	612	ATACCCTGTTGGTTGTAAAGTTTGCACGTGAGGGTTTGTGGAATTGGAGCCT	671
Db	301	ATACCCTGTTGGTTGTAAAGTTTGCACGTGAGGGTTTGTGGAATTGGAGCCT	360
Qy	672	AATTGATTTCATTCTTATTCATGCAGATTGTTGGACCTTCAGATGGAAGTAGTTACAT	731
Db	361	AATTGATTTCATTCTTATTCATGCAGATTGTTGGACCTTCAGATGGAAGTAGTTACAT	420
Qy	732	TATAGATTACTATGGAACCAGACTTACAAGACTGAGTATTACTAATGAAACATTAGAAA	791
Db	421	TATAGATTACTATGGAACCAGACTTACAAGACTGAGTATTACTAATGAAACATTAGAAA	480
Qy	792	AACGCAATTATCCATAA	810
Db	481	AACGCAATTATCCATAA	499

RESULT 3
US-09-276-531-33
; Sequence 33, Application US/09276531
; Patent No. 6183968
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Lal, Preeti
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Yue, Henry
; APPLICANT: Reddy, Roopa
; APPLICANT: Guegler, Karl J.
; APPLICANT: Baughn, Mariah R.
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF GENES ENCODING
; TITLE OF INVENTION: RECEPTORS AND PROTEINS ASSOCIATED WITH CELL
PROLIFERATION
; NUMBER OF SEQUENCES: 134
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/276,531
; FILING DATE: Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/079,677
; FILING DATE: March 27, 1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Lynn E. Murry, Ph.D.
; REGISTRATION NUMBER: 42,918
; REFERENCE/DOCKET NUMBER: PA-0008 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1455 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: BRAITUT01
; CLONE: 746308

US-09-276-531-33

Query Match 6.18; Score 49.8; DB 3; Length 1455;
Best Local Similarity 51.1%; Pred. No. 7.8e-06;
Matches 117; Conservative 0; Mismatches 112; Indels 0; Gaps 0;

RESULT 4

US-09-489-039A-6022

; Sequence 6022, Application US/09489039A

; Patent No. 6610836

; GENERAL INFORMATION:

; APPLICANT: Gary Breton et. al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO

KLEBSIELLA

• TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 2709.2004001

CURRENT APPLICATION NUMBER: US/09/489,039A

CURRENT FILING DATE: 2000-01-27

PCT/US2003/020000 PCTOR APPLICATION NUMBER: US 60/117,747

PRIOR FILING DATE: 1999-01-29

NUMBER OF SEO ID NOS: 14342

SEQ ID NO 6022

; LENGTH: 1119

; TYPE: DNA

ORGANISM: *Klebsiella pneumoniae*

US-09-489-039A-6022

Query Match 5.0%; Score 40.4; DB 4; Length 1119;
Best Local Similarity 50.0%; Pred. No. 0.0079;
Matches 101; Conservative 0; Mismatches 101; Indels 0; Gaps 0;

Qy	105	GAACCTCGCCCTGTTGCCCTTCTCCCTCCCGCTCCTGGGCGGAGGCGGAAGCGGAAGTGG	164
Dy	672	GAACAGCGGGCGGTTCCTCGGCGCGCCGACGCCCTGAACAAACGGCGTGTGGAGAGTAG	731

Qy 165 CGAGAAA GTGCGGTCTCCAAGATGGCGGCCGCGCTGGCGTCTGGTCCGTCTGCTCCGGA 224
 ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 Db 732 CGAACCCAGCGGGCAGCCGCCGCGACGGCTCTGCCGCCGGCGCACGCCAACAGCGCCAGT 791

Qy 225 GGCCGTGACGGCCAGACTCGTTGGTGTCTGTGGTTCGTCTCACTACAGGACCCTG 284
 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 Pb 792 GACCGGCCCTGGCTCCATTCAAGGGTAATGTGGCAGCCGCTGCGGCCACCGCCGCAGCCGC 851

QY 285 GGGGGCTGTTGCCACCTCCGCC 306

Db 852 TGGCGCCGTGGCGGCCTCGTCC 873

RESULT 5
US-10-027-983-11
; Sequence 11, Application US/10027983
; Patent No. 6617162
; GENERAL INFORMATION:
; APPLICANT: Kenneth W. Dobie
; APPLICANT: Mark P. Roach
; TITLE OF INVENTION: ANTISENSE MODULATION OF ESTROGEN RECEPTOR ALPHA
EXPRESSION
; FILE REFERENCE: RTS-0340
; CURRENT APPLICATION NUMBER: US/10/027,983
; CURRENT FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 98
; SEQ ID NO 11
; LENGTH: 392000
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 137740
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 137742
; OTHER INFORMATION: unknown
; NAME/KEY: misc_feature
; LOCATION: (138122)...(138221)
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: unsure
; LOCATION: 145507
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 151967
; OTHER INFORMATION: unknown
; NAME/KEY: misc_feature
; LOCATION: (151967)...(1542066)
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: unsure
; LOCATION: 154217
; OTHER INFORMATION: unknown
; NAME/KEY: misc_feature
; LOCATION: (164037)...(164136)
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: misc_feature
; LOCATION: (174657)...(174756)
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: misc_feature
; LOCATION: (186224)...(186323)
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: misc_feature
; LOCATION: (195242)...(195341)
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: unsure
; LOCATION: 202703
; OTHER INFORMATION: unknown

; NAME/KEY: misc_feature
; LOCATION: (202771)...(202870)
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: misc_feature
; LOCATION: (206246)...(215602)
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: misc_feature
; LOCATION: (218126)...(218225)
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: misc_feature
; LOCATION: (220360)...(220459)
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: misc_feature
; LOCATION: (222717)...(222816)
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: misc_feature
; LOCATION: (223981)...(224080)
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: misc_feature
; LOCATION: (227487)...(227586)
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: misc_feature
; LOCATION: (230157)...(230256)
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: misc_feature
; LOCATION: (232299)...(232398)
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: misc_feature
; LOCATION: (236552)...(2366651)
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: exon
; LOCATION: (118288)...(119101)
; OTHER INFORMATION: exon 1C
; NAME/KEY: exon:inton junction
; LOCATION: (151129)...(151130)
; OTHER INFORMATION: exon 5:inton 5
; NAME/KEY: exon:inton junction
; LOCATION: (299248)...(299249)
; OTHER INFORMATION: exon 9:inton 9
; NAME/KEY: exon:inton junction
; LOCATION: (348578)...(348579)
; OTHER INFORMATION: exon 10:inton 10
; NAME/KEY: inton
; LOCATION: (348579)...(381838)
; OTHER INFORMATION: inton 10
; NAME/KEY: inton:exon junction
; LOCATION: (386185)...(386186)
; OTHER INFORMATION: inton 11:exon 12

US-10-027-983-11

Query Match 4.8%; Score 38.6; DB 4; Length 392000;
Best Local Similarity 54.6%; Pred. No. 1.5;
Matches 77; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

Db 676281 ACCCCACGTCCCGGTAGCGCCGGCTGCCGCCGTCACCGGGAGCTCCGCCGTACCGCCGCT
676340

Qy 292 GTTGCCACCTCCGCCGGGGCGAGGAGTCGCTTAAGTGCAGGA 335
||||| | ||||| | ||| | | ||| |
Db 676341 ACCGCCAGCCCCGCCGGCGCCGGCTGCCGCCGAGGCCGAGCA 676384

RESULT 7

US-08-552-142A-16

; Sequence 16, Application US/08552142A

; Patent No. 5695995

; GENERAL INFORMATION:

; APPLICANT: Weintraub, Harold M.

; APPLICANT: Lee, Jacqueline E.

; APPLICANT: Tapscott, Stephen J.

; APPLICANT: Hollenberg, Stanley M.

; TITLE OF INVENTION: Neurogenic Differentiation (NeuroD) Genes

; TITLE OF INVENTION: and Proteins

; NUMBER OF SEQUENCES: 20

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Christensen O'Connor Johnson Kindness PLLC

; STREET: 1420 Fifth Avenue, Suite 2800

; CITY: Seattle

; STATE: WA

; COUNTRY: USA

; ZIP: 98101-2347

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/552,142A

; FILING DATE: 02-NOV-1995

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/239,238

; FILING DATE: 06-MAY-1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: WO PCT/US95/05741

; FILING DATE: 08-MAY-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Broderick, Thomas F.

; REGISTRATION NUMBER: 31,332

; REFERENCE/DOCKET NUMBER: FHCR-1-8933

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 206-682-8100

; TELEFAX: 206-225-0709

; INFORMATION FOR SEQ ID NO: 16:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1462 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

; ORIGINAL SOURCE:

; ORGANISM: Mus musculus
; IMMEDIATE SOURCE:
; CLONE: 1.1.1
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 231..1101
US-08-552-142A-16

Query Match 4.5%; Score 36.4; DB 1; Length 1462;
Best Local Similarity 49.0%; Pred. No. 0.19;
Matches 97; Conservative 0; Mismatches 101; Indels 0; Gaps 0;

QY 121 CCCTTCTCCCTCCGCTCCTGGCGGAGGCGGAAGCGGAAGTGGCGAGAAAGTGTGGTC 180
| | | || | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 261 CTCCCTCGGACGTGCCAAGTTGCCAGCTGGGCGACGGCGACGACGAGGCCGAGG 320

QY 181 TCCAAGATGGCGGCCGCCTGGCGTCTGGTCCGTCTGCTCCGGAGGCCGTGACGCCAGA 240
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 321 AGCGACAAGGGCGACGCCGCCGCAGCCTCTCCTGCTCCGGGTGCCCCCTCCAGGA 380

QY 241 CTCGTTGGTGTCCCTGTGGTCGTCTCAGTCACTACAGGACCCCTGGGGGGCTGTTGCCACC 300
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 381 CCCGCCGGGCCGCCAAGCCAGTGTCTCTCGTGGAGGAGAAGAGATCCCTGAACCCACG 440

QY 301 TCCGCCGGGGCGAGGAG 318
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 441 TTGGCTGAGGTCAAGGAG 458

RESULT 8

US-08-910-973-16

; Sequence 16, Application US/08910973
; Patent No. 5795723
; GENERAL INFORMATION:
; APPLICANT: Tapscott, Stephen J.
; APPLICANT: Olson, James M.
; TITLE OF INVENTION: Expression of Neurogenic bHLH Genes in Primitive
Neuroectoder
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Christensen O'Connor Johnson Kindness PLLC
; STREET: 1420 Fifth Avenue, Suite 2800
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101-2347
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/910,973
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/239,238

; FILING DATE: 06-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US95/05741
; FILING DATE: 08-MAY-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/17532
; FILING DATE: 30-October-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Sheiness, Diana K.
; REGISTRATION NUMBER: 35,356
; REFERENCE/DOCKET NUMBER: FHCR-1-10958
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-682-8100; 206-224-0735 (direct)
; TELEFAX: 206-225-0779
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1951 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Mus musculus
; IMMEDIATE SOURCE:
; CLONE: 1.1.1 (mouse neuroD2)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 230..1378
US-08-910-973-16

Query Match 4.5%; Score 36.4; DB 1; Length 1951;
Best Local Similarity 49.0%; Pred. No. 0.23;
Matches 97; Conservative 0; Mismatches 101; Indels 0; Gaps 0;

Qy	121	CCCTTCTCCCTCCCCTGGCGGAGGCCGAAGCGGAAGTGGCAGAAAGTGTGGTC 180
Db	260	CTCCTCTCGGACGTGCCCAAGTTGCCAGCTGGGCGACGGCGACGACGAGCCGAGG 319
Qy	181	TCCAAGATGGCGGCCCTGGCGTCTGGTCCGTCTGCTCCGGAGGCCGTGACGCCAGA 240
Db	320	AGCGACAAGGGCGACGCCGCCAGCCTCTGCTCCGGGTCGGGGCTCCAGGA 379
Qy	241	CTCGTTGGTGCCTGTGGTTCGTCTCAGTCACTACAGGACCCCTGGGGGCTGTTGCCACC 300
Db	380	CCCGCCCGGGCGCCAAGCCAGTGTCTTCTGGAGGAGAAGAGATCCCTGAACCCACG 439
Qy	301	TCCGCCGGGGCGAGGAG 318
Db	440	TTGGCTGAGGTCAAGGAG 457

RESULT 9
US-09-499-227-16
; Sequence 16, Application US/09499227
; Patent No. 6444463
; GENERAL INFORMATION:
; APPLICANT: Tapscott, Stephen J.

; APPLICANT: Olson, James M.
; TITLE OF INVENTION: Expression of Neurogenic bHLH Genes in Primitive
Neuroectoder
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Christensen O'Connor Johnson Kindness PLLC
; STREET: 1420 Fifth Avenue, Suite 2800
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101-2347
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/499,227
; FILING DATE: 05-August-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/239,238
; FILING DATE: 06-May-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US95/05741
; FILING DATE: 08-May-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/17532
; FILING DATE: 30-October-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/910,973
; FILING DATE: 07-August-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Sheiness, Diana K.
; REGISTRATION NUMBER: 35,356
; REFERENCE/DOCKET NUMBER: FHCR-1-12742
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-682-8100; 206-224-0735 (direct)
; TELEFAX: 206-225-0779
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1951 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Mus musculus
; IMMEDIATE SOURCE:
; CLONE: 1.1.1 (mouse neuroD2)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 230..1378

US-09-499-227-16

Query Match 4.5%; Score 36.4; DB 4; Length 1951;
Best Local Similarity 49.0%; Pred. No. 0.23;
Matches 97; Conservative 0; Mismatches 101; Indels 0; Gaps 0;

; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 12291
; LENGTH: 1404
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-12291

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Query Match           4.4%; Score 35.4; DB 4; Length 1404;
Best Local Similarity 48.3%; Pred. No. 0.4;
Matches 99; Conservative 0; Mismatches 106; Indels 0; Gaps 0;

Qy      60 GCGAAGAGACGGAACTGGCCTCTATCCTATGCGAGGTCCCTTAAGAACCTCGCCCTGTT 119
        ||||| | | | | | | | | | | | | | | | | | | | | | | |
Db      1324 GCGCAGCCAGGTCAACCACCTGACCCGCCCTGCGTCGCGAGGCGCAGGCCGATCCGGT 1265

Qy      120 GCCCTTCTCCCTCCCGCTCCTGGCGGAGGCAGGAAGCGGAAGTGGCGAGAAAGTGTGGT 179
        || | | | | | | | | | | | | | | | | | | | | | | |
Db      1264 GCAATTCTCGCAACTGGTCGTGCTTGGCGCGATCGACCGCCTTGGCGGCACGTCACACC 1205

Qy      180 CTCCAAGATGGCGGCCGCCTGGCGTCTGGTCCGTCTGCTCCGGAGGCCGTGACGGCCAG 239
        || | | | | | | | | | | | | | | | | | | | | | | |
Db      1204 TTCCGAGCTGGCGCCGCCGAGCGGATGCGCTCGTCAATCTGGCCGCGCTGCTGCGCGA 1145

Qy      240 ACTCGTTGGTGTCCGTGGTC 264
        || | | | | | | | | | | |
Db      1144 ACTGGAACCGCGGAGGGCTGATCGTC 1120

```

RESULT 13

US-10-204-708-36

; Sequence 36, Application US/10204708

; Patent No. 6677731

; GENERAL INFORMATION:

; APPLICANT: OLEK, Alexander

; APPLICANT: PIE

; APPLICANT: BERLIN,

; TITLE OF INVENTION: Diagnosis of D

; TITLE OF INVENTION: by Assessing DNA Methylation

; FILE REFERENCE: 5013.1012

; CURRENT APPLICATION NUMBER

; CURRENT FILING DATE: 2003-05-06

PRIOR APPLICATION NUMBER: PCT/EP

; PRIOR FILING DATE: 2001-04-06

PRIOR APPLICATION NUMBER: DE 10019058

; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 98
; SEQ ID NO 36
; LENGTH: 9347
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-204-708-36

Query Match 4.4%; Score 35.4; DB 4; Length 9347;
Best Local Similarity 45.7%; Pred. No. 1.4;
Matches 123; Conservative 0; Mismatches 146; Indels 0; Gaps 0;

Qy 535 AATGGCTATT CCTACAAAGTGGCAGTCGCATT GTCTCTTTCTTGGATGGTTGGGAGCA 594
||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| |
Db 7248 AATAGTAGTTGAGATAAAATAGAAGTTATT TTTTCGTTAGATAAAATAATT TAGAGA 7307

Qy 595 GATCGATTTACCTTGGATACCC TGCTTGTTGTAAAGTTGC ACTGTAGGGTT 654
| | | ||| | | | ||| | ||| | ||| | ||| | | | |
Db 7308 TAGGTAGTTAGGGTAAATGGTGGTTACGTTATTAGGTTTATCGTTTATT 7367

Qy 655 TGTGGAATTGGGAGCCTAATTGATTCAATTCTTATTTCAATGCAGATTGTTGGACCTCA 714
| | | | | | | ||| | ||| | | | | | | | | | |
Db 7368 ATTGTTTCGAATTAATT TTATTTAGTTATTAGTTATTGTTAAGATGGTTTGGGA 7427

Qy 715 GATGGAAGTAGTTACATTATAGATTACTATGGAACCAGACTTACAAGACTGAGTATTACT 774
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Db 7428 ATTTAGTTATTAGATTATTTATTAGGTAGCGGAAAGTAGGAAGAAGAAAGGGT 7487

Qy 775 AATGAAACATTAGAAAAACGCAATTATA 803
| | | | | | ||| | | | | |
Db 7488 AAATAAAATT TAAAGATAAGTAAGA 7516

RESULT 14

US-08-545-528D-1
; Sequence 1, Application US/08545528D
; Patent No. 6537773
; GENERAL INFORMATION:

; APPLICANT: Fraser et al.
; TITLE OF INVENTION: Nucleotide Sequence of the Mycoplasma Genitalium Genome,
Fragments
; Patent No. 6537773
; TITLE OF INVENTION: Thereof, and Uses Thereof
; FILE REFERENCE: PB193P1
; CURRENT APPLICATION NUMBER: US/08/545,528D
; CURRENT FILING DATE: 1995-10-19
; PRIOR APPLICATION NUMBER: US 08/488,018
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: US 08/473,545

; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 580073
; TYPE: DNA
; ORGANISM: Mycoplasma genitalium
US-08-545-528D-1

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Query Match           4.4%; Score 35.4; DB 4; Length 580073;
Best Local Similarity 55.2%; Pred. No. 21;
Matches 69; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

Qy      685 CTTATTCATGCAGATTGTTGGACCTTCAGATGGAAGTAGTTACATTATAGATTACTAT 744
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Db      387060 CTTTTTAAAGTTAAATTGTCTGCTTGTGAATCCATGGTAAGCAGGATGGAATTATTA
387119

Qy      745 GGAACCAGACTTACAAGACTGAGTATTACTAATGAAACATTAGAAAAACGCAATTATAT 804
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Db      387120 AGTACCTTCCATCCAAGGCTTATTATGAATCATTAAACAATAAGCAAATTCAATTAAAG
387179

Qy      805 CCATA 809
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Db      387180 CCATA 387184

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RESULT 15

US-09-103-840A-1
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4411529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1

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Best Local Similarity 47.3%; Pred. No. 66;
Matches 106; Conservative 0; Mismatches 118; Indels 0; Gaps 0;
Qy      112 GCCCTGTTGCCCTCTCCCTCCGCTCCTGGCGAGGCAGCGGAAGCGGAAGTGGCAGAAA 171
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Db      674718 GCCGGGCGCGCCGTTCGCGCCATGCGCGCTGCCGCCAGCCTGGCGCCACCGCGCCACC
674777

Qy      172 GTGTCGGTCTCCAAGATGGCGGCCGCCTGGCGCTGGTCCGTCTGCTCCGGAGGCCGTG 231
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Db      674778 GGCCCCACCGGCGCCCGGGTTGCCGCCATTGCCACCGGTCCCGCCGGCACCAAGGTTGTG
674837

Qy      232 ACGGCCAGACTCGTTGGTGTCCGTGGTCGTCTCAGTCACTACAGGACCTGGGGGCT 291
        || | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      674838 ACCCCCACGTCCCGGTAGCGCCGTTGCCGCCGTACCGGGAGCTCCGCCGTACCGCCGCT
674897

Qy      292 GTTGCCACCTCCGCCGGGGCGAGGAGTCGCTTAAGTGCAGGA 335
        || | | | | | | | | | | | | | | | | | | | | | | | |
Db      674898 ACCGCCAGCCCCGCCGGCGCCGTTGGCTGCCGCCAGGGCCGAGCA 674941

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Search completed: March 4, 2004, 09:18:33
Job time : 106 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 4, 2004, 08:34:04 ; Search time 349 Seconds
(without alignments)
8488.596 Million cell updates/sec

Title: US-09-852-100B-1

Perfect score: 810

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2421054 seqs, 1828716029 residues

Total number of hits satisfying chosen parameters: 4842108

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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17: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*

18: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

8

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2	810	100.0	810	9	US-09-833-503A-1	Sequence 1, Appli	
3	810	100.0	810	14	US-10-199-881-1	Sequence 1, Appli	
4	499	61.6	508	9	US-09-922-217-233	Sequence 233, App	
5	499	61.6	508	9	US-09-922-217-245	Sequence 245, App	
6	499	61.6	508	9	US-09-833-263-233	Sequence 233, App	
7	499	61.6	508	9	US-09-833-263-245	Sequence 245, App	
8	499	61.6	508	13	US-10-025-380-233	Sequence 233, App	
9	499	61.6	508	13	US-10-025-380-245	Sequence 245, App	
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12	100	12.3	256	15	US-10-242-535A-36056	Sequence 36056, A	
13	85.4	10.5	411	12	US-10-085-783A-48351	Sequence 48351, A	
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15	79	9.8	129	12	US-10-085-783A-16414	Sequence 16414, A	
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20	51	6.3	1369	10	US-09-305-736-102	Sequence 102, App	
21	51	6.3	1369	11	US-09-818-683-102	Sequence 102, App	
22	51	6.3	1369	12	US-10-621-401-102	Sequence 102, App	
23	50.4	6.2	854	10	US-09-796-753-49	Sequence 49, Appl	
c	24	50.2	6.2	439	9	US-09-917-800A-829	Sequence 829, App
	25	49.8	6.1	746	9	US-09-833-503A-5	Sequence 5, Appli
	26	49.8	6.1	746	14	US-10-199-881-5	Sequence 5, Appli
	27	49.8	6.1	1406	10	US-09-992-600A-81	Sequence 81, Appl
	28	49.8	6.1	1406	10	US-09-924-340-81	Sequence 81, Appl
	29	49.8	6.1	1406	10	US-09-992-095B-81	Sequence 81, Appl
	30	49.8	6.1	1406	10	US-09-999-570-81	Sequence 81, Appl
	31	49.8	6.1	1406	14	US-10-000-489-81	Sequence 81, Appl
	32	49.8	6.1	1406	14	US-10-000-986-81	Sequence 81, Appl
	33	49.8	6.1	1406	14	US-10-154-678-81	Sequence 81, Appl
	34	49.8	6.1	1406	14	US-10-001-142-81	Sequence 81, Appl
	35	49.8	6.1	1473	10	US-09-796-753-47	Sequence 47, Appl
	36	49.8	6.1	1481	14	US-10-198-846-11017	Sequence 11017, A
	37	48.8	6.0	423	14	US-10-198-846-8649	Sequence 8649, Ap
c	38	42.2	5.2	559	15	US-10-027-632-197570	Sequence 197570,
	39	41.2	5.1	12592	12	US-10-221-613-58	Sequence 58, Appl
	40	39.8	4.9	909	14	US-10-156-761-6614	Sequence 6614, Ap
	41	39.8	4.9	962	9	US-09-833-503A-3	Sequence 3, Appli
	42	39.8	4.9	962	14	US-10-199-881-3	Sequence 3, Appli
	43	39.8	4.9	1409	9	US-09-925-301-176	Sequence 176, App
	44	39.8	4.9	1422	10	US-09-798-889-24	Sequence 24, Appl
	45	39.8	4.9	1422	12	US-10-633-680-24	Sequence 24, Appl

ALIGNMENTS

RESULT 1

US-09-852-100A-1

; Sequence 1, Application US/09852100A

; Patent No. US20020058267A1

; GENERAL INFORMATION:

; APPLICANT: American Home Products

; TITLE OF INVENTION: Beta-amyloid Peptide-Binding Proteins and Polynucleotides
Encoding the
; TITLE OF INVENTION: Same
; FILE REFERENCE: AHP981261p2
; CURRENT APPLICATION NUMBER: US/09/852,100A
; CURRENT FILING DATE: 2001-05-09
; PRIOR APPLICATION NUMBER: US 09/172,990
; PRIOR FILING DATE: 1998-10-14
; PRIOR APPLICATION NUMBER: US 60/104,104
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: PTC/US99/21621
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: US 09/060,609
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: US 60/064,583
; PRIOR FILING DATE: 1997-04-16
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 810
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(807)
US-09-852-100A-1

Query Match 100.0%; Score 810; DB 9; Length 810;
Best Local Similarity 100.0%; Pred. No. 1.8e-244;
Matches 810; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGCATATTAAAGGTCTCCCAATGTGATTCCACGGCTCACGGCAGAACACG 60
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Qy 61 CGAAGAGACGGAACCTGGCCTATCCTATGCGAGGTCCCTTAAGAACCTGCCCTGTTG 120

Db 121 CCCTTCTCCCTCCGCTCCTGGCGGAGGCAGAAGCAGAAGTGGCAGAAAGTGTGGTC 180

Qy 181 TCCAAGATGGCGGCCCTGGCGTCTGGTCCGTCTGCTCCGGAGGCCGTGACGGCCAGA 240
Pb 181 TCCAAGATGGCGGCCCTGGCGTCTGGTCCGTCTGCTCCGGAGGCCGTGACGGCCAGA 240

Qy 241 CTCGTTGGTGTCTGTGGGTCGTCTCAGTCACTACAGGACCCTGGGGGGCTGTTGCCACC 300

Qy 301 TCCGCCGGGGCGAGGAGTCGCTTAAGTGCAGGACCTCAAAGTGGGACAATATATTGT 360

Db 301 TCCGCCGGGGCGAGGAGTCGCTTAAGTGCAGGACCTCAAAGTGGGACAATATATTGT 360

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Db	361 AAAGATCCAAAATAATGACGCTACGCAAGAACCAAGCTTAACGTACAAACTACACAGCT	420
Qy	421 CATTTTCTGTTCCAGCACCAACATAACTTGTAAAGGATTCCAGTGGCAATGAAACA	480
Db	421 CATTTTCTGTTCCAGCACCAACATAACTTGTAAAGGATTCCAGTGGCAATGAAACA	480
Qy	481 CATTACTGGAACGAAGTTGGTTTTCAAGCCCATACTTGCAGCGAAATGTAAATGGC	540
Db	481 CATTACTGGAACGAAGTTGGTTTTCAAGCCCATACTTGCAGCGAAATGTAAATGGC	540
Qy	541 TATTCTACAAAGTGGCAGTCGATTGTCTTTTCTGGATGGTGGAGCAGATCGA	600
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Db	601 TTTTACCTGGATACCCTGCTTGGTTAAAGTTTGCAGTGTAGGGTTTGGA	660
Qy	661 ATTGGGAGCCTAATTGATTCATTCTTATTCAATGCAGATTGGACCTTCAGATGGA	720
Db	661 ATTGGGAGCCTAATTGATTCATTCTTATTCAATGCAGATTGGACCTTCAGATGGA	720
Qy	721 AGTAGTTACATTATAGATTACTATGAAACCAGACTTACAAGACTGAGTATTACTAATGAA	780
Db	721 AGTAGTTACATTATAGATTACTATGAAACCAGACTTACAAGACTGAGTATTACTAATGAA	780
Qy	781 ACATTTAGAAAAACGCAATTATATCCATAA	810
Db	781 ACATTTAGAAAAACGCAATTATATCCATAA	810

RESULT 2

US-09-833-503A-1

; Sequence 1, Application US/09833503A

; Patent No. US20020146760A1

; GENERAL INFORMATION:

; APPLICANT: Ozenberger, Bradley A

; APPLICANT: Kajkowski, Eileen M

; APPLICANT: Lo, Ching-Hsiung F

; APPLICANT: American Home Products Corporation

; TITLE OF INVENTION: No. US20020146760A1 G-Protein-Coupled Receptor-Like Proteins and

; TITLE OF INVENTION: Polynucleotides Encoded By Them, and Methods of Using

; TITLE OF INVENTION: Same

; FILE REFERENCE: AHP98165-00PCT

; CURRENT APPLICATION NUMBER: US/09/833,503A

; CURRENT FILING DATE: 2000-10-13

; PRIOR APPLICATION NUMBER: 60/104,104

; PRIOR FILING DATE: 1998-10-13

; NUMBER OF SEQ ID NOS: 6

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 1

; LENGTH: 810

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-833-503A-1

Query Match 100.0%; Score 810; DB 9; Length 810;
Best Local Similarity 100.0%; Pred. No. 1.8e-244;
Matches 810; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGCATATTTAAAAGGGTCTCCAATGTGATTCCACGGGCTCACGGCAGAACACG 60
Db 1 ATGCATATTTAAAAGGGTCTCCAATGTGATTCCACGGGCTCACGGCAGAACACG 60

Qy 61 CGAAGAGACGGAACCTGGCCTCTATCCTATGCGAGGTCCCTTAAGAACCTGCCCTGTTG 120
Db 61 CGAAGAGACGGAACCTGGCCTCTATCCTATGCGAGGTCCCTTAAGAACCTGCCCTGTTG 120

Qy 121 CCCTTCTCCCTCCCGCTCCTGGCGGAGGCGGAAGCGGAAGTGGCGAGAAAGTGTGGTC 180
Db 121 CCCTTCTCCCTCCCGCTCCTGGCGGAGGCGGAAGCGGAAGTGGCGAGAAAGTGTGGTC 180

Qy 181 TCCAAGATGGCGGCCGCCTGGCGTCTGGTCCGTCTGCTCCGGAGGCCGTGACGGCCAGA 240
Db 181 TCCAAGATGGCGGCCGCCTGGCGTCTGGTCCGTCTGCTCCGGAGGCCGTGACGGCCAGA 240

Qy 241 CTCGTTGGTGTCCGTGGTCGCTCAGTCACTACAGGACCTGGGGGCTGTTGCCACC 300
Db 241 CTCGTTGGTGTCCGTGGTCGCTCAGTCACTACAGGACCTGGGGGCTGTTGCCACC 300

Qy 301 TCCGCCGGGGCGAGGAGTCGCTTAAGTGCAGGACCTCAAAGTGGACAATATATTGT 360
Db 301 TCCGCCGGGGCGAGGAGTCGCTTAAGTGCAGGACCTCAAAGTGGACAATATATTGT 360

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Db 421 CATGTTCTGTTCCAGCACCCAACATAACTTGTAAAGGATTCCAGTGGCAATGAAACA 480

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Qy 541 TATTCCCTACAAAGTGGCAGTCGATTGTCTTTTCTTGGATGGTGGAGCAGATCGA 600
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Db 661 ATTGGGAGCCTAATTGATTCATTCTTATTCAATGCAGATTGGACCTTCAGATGGA 720

Qy 721 AGTAGTTACATTATAGATTACTATGGAACCAGACTTACAAGACTGAGTATTACTAATGAA 780
Db 721 AGTAGTTACATTATAGATTACTATGGAACCAGACTTACAAGACTGAGTATTACTAATGAA 780

Qy 781 ACATTTAGAAAAACGCAATTATATCCATAA 810

Db 781 ||||||| ACATTTAGAAAAACGCAATTATATCCATAA 810

RESULT 3

US-10-199-881-1

; Sequence 1, Application US/10199881
; Publication No. US20030096356A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: No. US20030096356A1 G-Protein-Coupled Receptor-Like Proteins and Polynucleotides
; TITLE OF INVENTION: Encoded by Them, and Methods of Using Same"
; FILE REFERENCE: AHP98165C1
; CURRENT APPLICATION NUMBER: US/10/199,881
; CURRENT FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: PCT/ US99/21621
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: US 90/833,5081
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: US 60/104,104
; PRIOR FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 810
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(810)
; OTHER INFORMATION:

US-10-199-881-1

Query Match 100.0%; Score 810; DB 14; Length 810;
Best Local Similarity 100.0%; Pred. No. 1.8e-244;
Matches 810; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 ATGCATATTAAAAGGGTCTCCAAATGTGATTCCACGGGCTCACGGGCAGAACACG 60

Qy 61 CGAAGAGACGGAACTGGCCTCTATCCTATGCGAGGTCCCTTAAGAACCTGCCCTGTTG 120
Db 61 CGAAGAGACGGAACTGGCCTCTATCCTATGCGAGGTCCCTTAAGAACCTGCCCTGTTG 120

Qy 121 CCCTTCTCCCTCCGCTCTGGCGGAGGCGGAAGCGGAAGTGGCGAGAAAGTGTGGTC 180
Db 121 CCCTTCTCCCTCCGCTCTGGCGGAGGCGGAAGCGGAAGTGGCGAGAAAGTGTGGTC 180

Qy 181 TCCAAGATGGCGGCCGCTGGCGTCTGGTCCGTCTGCTCCGGAGGCCGTGACGGCCAGA 240
Db 181 TCCAAGATGGCGGCCGCTGGCGTCTGGTCCGTCTGCTCCGGAGGCCGTGACGGCCAGA 240

Qy 241 CTCGTTGGTGTCTGTGGTCGTCTCAGTCACTACAGGACCTGGGGGCTGTTGCCACC 300
Db 241 CTCGTTGGTGTCTGTGGTCGTCTCAGTCACTACAGGACCTGGGGGCTGTTGCCACC 300

QY 301 TCCGCCGGGGCGAGGAGTCGCTTAAGTGCAGGACCTAAAGTGGACAATATATTGT 360
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Db 301 TCCGCCGGGGCGAGGAGTCGCTTAAGTGCAGGACCTAAAGTGGACAATATATTGT 360

QY 361 AAAGATCCAAAATAATGACGCTACGCAAGAACCAAGTTAAGTACAAACTACACAGCT 420
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Db 361 AAAGATCCAAAATAATGACGCTACGCAAGAACCAAGTTAAGTACAAACTACACAGCT 420

QY 421 CATGTTCTGTTCCAGCACCCAACATAACTGTAAGGATTCCAGTGGCAATGAAACA 480
|||
Db 421 CATGTTCTGTTCCAGCACCCAACATAACTGTAAGGATTCCAGTGGCAATGAAACA 480

QY 481 CATTACTGGAACGAAGTTGGTTTCAAGCCATATCTGCCGAAATGAAATGGC 540
|||
Db 481 CATTACTGGAACGAAGTTGGTTTCAAGCCATATCTGCCGAAATGAAATGGC 540

QY 541 TATTCTACAAAGTGGCAGTCGCATTGTCTCTTCTGGATGGTGGAGCAGATCGA 600
|||
Db 541 TATTCTACAAAGTGGCAGTCGCATTGTCTCTTCTGGATGGTGGAGCAGATCGA 600

QY 601 TTTTACCTGGATACCCTGCTTGGTTTGTAAAGTTGCAGTGAGGTTTGGA 660
|||
Db 601 TTTTACCTGGATACCCTGCTTGGTTTGTAAAGTTGCAGTGAGGTTTGGA 660

QY 661 ATTGGGAGCCTAATTGATTCATTCTTATTCAATGCAGATTGGACCTCAGATGGA 720
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Db 661 ATTGGGAGCCTAATTGATTCATTCTTATTCAATGCAGATTGGACCTCAGATGGA 720

QY 721 AGTAGTTACATTATAGATTACTATGGAACCAGACTTACAAGACTGAGTATTACTAATGAA 780
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Db 721 AGTAGTTACATTATAGATTACTATGGAACCAGACTTACAAGACTGAGTATTACTAATGAA 780

QY 781 ACATTTAGAAAAACGCAATTATATCCATAA 810
|||
Db 781 ACATTTAGAAAAACGCAATTATATCCATAA 810

RESULT 4

US-09-922-217-233

; Sequence 233, Application US/09922217

; Patent No. US20020076414A1

; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun
; APPLICANT: Lodes, Michael J.
; APPLICANT: Secrist, Heather
; APPLICANT: Benson, Darin R.
; APPLICANT: Meagher, Madeleine Joy
; APPLICANT: Stolk, John A.
; APPLICANT: Wang, Tongtong
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Smith, Carole Lynn
; APPLICANT: King, Gordon E.
; APPLICANT: Wang, Aijun
; APPLICANT: Clapper, Jonathan D.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE

; FILE REFERENCE: 210121.471C13
; CURRENT APPLICATION NUMBER: US/09/922,217
; CURRENT FILING DATE: 2001-08-03
; NUMBER OF SEQ ID NOS: 1124
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 233
; LENGTH: 508
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-922-217-233

Query Match 61.6%; Score 499; DB 9; Length 508;
Best Local Similarity 100.0%; Pred. No. 1.8e-146;
Matches 499; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	312 CGAGGAGTCGCTTAAGTGCAGGACCTCAAAGTGGACAATATATTGTAAAGATCCAAA	371
Db	1 CGAGGAGTCGCTTAAGTGCAGGACCTCAAAGTGGACAATATATTGTAAAGATCCAAA	60
Qy	372 AATAAATGACGCTACGCAAGAACCACTAACAGTTAACACTACACAGCTCATGTTCCCTG	431
Db	61 AATAAATGACGCTACGCAAGAACCACTAACAGTTAACACTACACAGCTCATGTTCCCTG	120
Qy	432 TTTTCCAGCACCCAACATAACTTGTAAAGGATCCAGTGGCAATGAAACACATTACTGG	491
Db	121 TTTTCCAGCACCCAACATAACTTGTAAAGGATCCAGTGGCAATGAAACACATTACTGG	180
Qy	492 GAACGAAGTTGGTTTTCAAGCCCATACTTGCCGAAATGTAAATGGCTATTCTACAA	551
Db	181 GAACGAAGTTGGTTTTCAAGCCCATACTTGCCGAAATGTAAATGGCTATTCTACAA	240
Qy	552 AGTGGCAGTCGATTGCTCTTTCTGGATGGTGGAGCAGATCGATTACCTTGG	611
Db	241 AGTGGCAGTCGATTGCTCTTTCTGGATGGTGGAGCAGATCGATTACCTTGG	300
Qy	612 ATACCCTGCTTGGTTGTAAAGTTGCACTGTAGGGTTGTGGAATTGGAGCCT	671
Db	301 ATACCCTGCTTGGTTGTAAAGTTGCACTGTAGGGTTGTGGAATTGGAGCCT	360
Qy	672 AATTGATTCATTCTATTCATGCAAGATTGTTGGACCTTCAGATGGAAGTAGTTACAT	731
Db	361 AATTGATTCATTCTATTCATGCAAGATTGTTGGACCTTCAGATGGAAGTAGTTACAT	420
Qy	732 TATAGATTACTATGGAACCAGACTTACAAGACTGAGTATTACTAATGAAACATTAGAAA	791
Db	421 TATAGATTACTATGGAACCAGACTTACAAGACTGAGTATTACTAATGAAACATTAGAAA	480
Qy	792 AACGCAATTATATCCATAA	810
Db	481 AACGCAATTATATCCATAA	499

RESULT 5

US-09-922-217-245

; Sequence 245, Application US/09922217

; Patent No. US20020076414A1

; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun
; APPLICANT: Lodes, Michael J.
; APPLICANT: Secrist, Heather
; APPLICANT: Benson, Darin R.
; APPLICANT: Meagher, Madeleine Joy
; APPLICANT: Stolk, John A.
; APPLICANT: Wang, Tongtong
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Smith, Carole Lynn
; APPLICANT: King, Gordon E.
; APPLICANT: Wang, Aijun
; APPLICANT: Clapper, Jonathan D.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.471C13
; CURRENT APPLICATION NUMBER: US/09/922,217
; CURRENT FILING DATE: 2001-08-03
; NUMBER OF SEQ ID NOS: 1124
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 245
; LENGTH: 508
; TYPE: DNA
; ORGANISM: Homo sapiens

US-09-922-217-245

Query Match 61.6%; Score 499; DB 9; Length 508;
Best Local Similarity 100.0%; Pred. No. 1.8e-146;
Matches 499; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	312 CGAGGAGTCGCTTAAGTGCAGGACCTCAAAGTGGACAATATATTGTAAAGATCCAAA	371
Db	1 CGAGGAGTCGCTTAAGTGCAGGACCTCAAAGTGGACAATATATTGTAAAGATCCAAA	60
Qy	372 AATAAATGACGCTACGCAAGAACCAAGTTAACTGTACAAACTACACAGCTCATGTTCCCTG	431
Db	61 AATAAATGACGCTACGCAAGAACCAAGTTAACTGTACAAACTACACAGCTCATGTTCCCTG	120
Qy	432 TTTTCCAGCACCCAACATAACTTGTAAGGATTCCAGTGGCAATGAAACACATTTACTGG	491
Db	121 TTTTCCAGCACCCAACATAACTTGTAAGGATTCCAGTGGCAATGAAACACATTTACTGG	180
Qy	492 GAACGAAGTTGGTTTTCAAGCCCATACTTGTAAAGTGGCTATTCTACAA	551
Db	181 GAACGAAGTTGGTTTTCAAGCCCATACTTGTAAAGTGGCTATTCTACAA	240
Qy	552 AGTGGCAGTCGATTGTCTTTTCTTGGATGGTGGAGCAGATCGATTACCTTGG	611
Db	241 AGTGGCAGTCGATTGTCTTTTCTTGGATGGTGGAGCAGATCGATTACCTTGG	300
Qy	612 ATACCCTGCTTGGTTTGTAAAGTTGCAGTGTAGGGTTGTGGAATTGGAGCCT	671
Db	301 ATACCCTGCTTGGTTGTAAAGTTGCAGTGTAGGGTTGTGGAATTGGAGCCT	360
Qy	672 AATTGATTCATTCTTATTCAATGCAGATTGTTGGACCTCAGATGGAAGTAGTTACAT	731
Db	361 AATTGATTCATTCTTATTCAATGCAGATTGTTGGACCTCAGATGGAAGTAGTTACAT	420

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Qy      732 TATAGATTACTATGGAACCAGACTTACAAGACTGAGTATTACTAATGAAACATTAGAAA 791
        ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||
Db      421 TATAGATTACTATGGAACCAGACTTACAAGACTGAGTATTACTAATGAAACATTAGAAA 480

Qy      792 AACGCAATTATATCCATAA 810
        ||||||| ||||||| |||||
Db      481 AACGCAATTATATCCATAA 499

```

RESULT 6

US-09-833-263-233

```

; Sequence 233, Application US/09833263
; Patent No. US20020110547A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Aijun
; APPLICANT: Clapper, Jonathan D.
; APPLICANT: Stolk, John A.
; APPLICANT: Meagher, Madeleine J.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF COLON CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.471C12
; CURRENT APPLICATION NUMBER: US/09/833,263
; CURRENT FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 233
; LENGTH: 508
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-833-263-233

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Query Match          61.6%;  Score 499;  DB 9;  Length 508;
Best Local Similarity 100.0%;  Pred. No. 1.8e-146;
Matches 499;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

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Qy      312 CGAGGGAGTCGCTTAAGTGCAGGGACCTCAAAGTGGGACAATATATTGTAAAGATCCAAA 371
        ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||
Db      1 CGAGGGAGTCGCTTAAGTGCAGGGACCTCAAAGTGGGACAATATATTGTAAAGATCCAAA 60

Qy      372 AATAAATGACGCTACGCAAGAACCGAGTTAAGTACAAACTACACAGCTCATGTTCCCTG 431
        ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||
Db      61 AATAAATGACGCTACGCAAGAACCGAGTTAAGTACAAACTACACAGCTCATGTTCCCTG 120

Qy      432 TTTTCCAGCACCCAACATAACTTGTAAGGATTCCAGTGGCAATGAAACACATTTACTGG 491
        ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||
Db      121 TTTTCCAGCACCCAACATAACTTGTAAGGATTCCAGTGGCAATGAAACACATTTACTGG 180

Qy      492 GAACGAAGTTGGTTTTCAAGCCCATACTGCCGAAATGTAAATGGCTATTCTACAA 551
        ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||
Db      181 GAACGAAGTTGGTTTTCAAGCCCATACTGCCGAAATGTAAATGGCTATTCTACAA 240

Qy      552 AGTGGCAGTCGCATTGTCTCTTTCTGGATGGTGGGAGCAGATCGATTTACCTGG 611
        ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||
Db      241 AGTGGCAGTCGCATTGTCTCTTTCTGGATGGTGGGAGCAGATCGATTTACCTGG 300

Qy      612 ATACCCCTGCTTGGTTGTTAAAGTTGCAGTGTAGGGTTGTGGAATTGGGAGCCT 671
        ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||

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Db	301 ATACCCTGCTTGGGTTGTTAAAGTTGCAGATTGTGGACCTTCAGATGGAAGTAGTTACAT	360
Qy	AATTGATTCATTCTTATTCAATGCAGATTGTGGACCTTCAGATGGAAGTAGTTACAT	731
Db	AATTGATTCATTCTTATTCAATGCAGATTGTGGACCTTCAGATGGAAGTAGTTACAT	420
Qy	TATAGATTACTATGGAACCAGACTACAAGACTGAGTATTACTAATGAAACATTAGAAA	791
Db	TATAGATTACTATGGAACCAGACTACAAGACTGAGTATTACTAATGAAACATTAGAAA	480
Qy	AACGCAATTATATCCATAA	810
Db	AACGCAATTATATCCATAA	499

RESULT 7

US-09-833-263-245

; Sequence 245, Application US/09833263

; Patent No. US20020110547A1

; GENERAL INFORMATION:

; APPLICANT: Wang, Aijun

; APPLICANT: Clapper, Jonathan D.

; APPLICANT: Stolk, John A.

; APPLICANT: Meagher, Madeleine J.

; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND

; TITLE OF INVENTION: DIAGNOSIS OF COLON CANCER AND METHODS FOR THEIR USE

; FILE REFERENCE: 210121.471C12

; CURRENT APPLICATION NUMBER: US/09/833,263

; CURRENT FILING DATE: 2001-04-10

; NUMBER OF SEQ ID NOS: 1093

; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO 245

; LENGTH: 508

; TYPE: DNA

; ORGANISM: Homo sapien

US-09-833-263-245

Query Match 61.6%; Score 499; DB 9; Length 508;
 Best Local Similarity 100.0%; Pred. No. 1.8e-146;
 Matches 499; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	312 CGAGGAGTCGCTTAAGTGCAGGACCTCAAAGTGGACAATATATTGTAAAGATCCAA	371

Db	1 CGAGGAGTCGCTTAAGTGCAGGACCTCAAAGTGGACAATATATTGTAAAGATCCAA	60
----	--	----

Qy	372 AATAAATGACGCTACGCAAGAACCGAGTTAACGTACAAACTACACAGCTCATGTTCTG	431

Db	61 AATAAATGACGCTACGCAAGAACCGAGTTAACGTACAAACTACACAGCTCATGTTCTG	120
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Qy	432 TTTCCAGCACCAACATAACTTGTAAGGATCCAGTGGCAATGAAACACATTACTGG	491

Db	121 TTTCCAGCACCAACATAACTTGTAAGGATCCAGTGGCAATGAAACACATTACTGG	180
----	---	-----

Qy	492 GAACGAAGTTGGTTTCAAGCCATATCTGCCGAAATGTAAATGGCTATTCCCTACAA	551

Db	181 GAACGAAGTTGGTTTCAAGCCATATCTGCCGAAATGTAAATGGCTATTCCCTACAA	240
----	--	-----

Qy 552 AGTGGCAGTCGCATTGCTCTTTCTGGATGGTGGGAGCAGATCGATTACCTGG 611
|||
Db 241 AGTGGCAGTCGCATTGCTCTTTCTGGATGGTGGGAGCAGATCGATTACCTGG 300

Qy 612 ATACCCTGCTTGGGTTGTTAAAGTTGCAGTGACTGTAGGGTTGTGGAATTGGGAGCCT 671
|||
Db 301 ATACCCTGCTTGGGTTGTTAAAGTTGCAGTGACTGTAGGGTTGTGGAATTGGGAGCCT 360

Qy 672 AATTGATTCATTCTTATTCAATGCAGATTGGACCTTCAGATGGAAGTAGTTACAT 731
|||
Db 361 AATTGATTCATTCTTATTCAATGCAGATTGGACCTTCAGATGGAAGTAGTTACAT 420

Qy 732 TATAGATTACTATGGAACCAGACTACAAGACTGAGTATTACTAATGAAACATTTAGAAA 791
|||
Db 421 TATAGATTACTATGGAACCAGACTACAAGACTGAGTATTACTAATGAAACATTTAGAAA 480

Qy 792 AACGCAATTATATCCATAA 810
|||
Db 481 AACGCAATTATATCCATAA 499

RESULT 8

US-10-025-380-233

; Sequence 233, Application US/10025380
; Publication No. US20020182191A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Lodes, Michael J.
; APPLICANT: Secrist, Heather
; APPLICANT: Benson, Darin R.
; APPLICANT: Meagher, Madeleine Joy
; APPLICANT: Stolk, John A.
; APPLICANT: Wang, Tongtong
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Smith, Carole L.
; APPLICANT: King, Gordon E.
; APPLICANT: Wang, Aijun
; APPLICANT: Clapper, Jonathan D.
; APPLICANT: Skeiky, Yasir A. W.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick Thomas S.
; APPLICANT: Carter, Darrick
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.471C14
; CURRENT APPLICATION NUMBER: US/10/025,380
; CURRENT FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 1129
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 233
; LENGTH: 508
; TYPE: DNA
; ORGANISM: Homo sapiens

US-10-025-380-233

Query Match 61.6%; Score 499; DB 13; Length 508;
Best Local Similarity 100.0%; Pred. No. 1.8e-146;

Matches 499; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	312	CGAGGAGTCGCTTAAGTGCAGGACCTCAAAGTGGACAATATATTGTAAAGATCCAAA	371
Db	1	CGAGGAGTCGCTTAAGTGCAGGACCTCAAAGTGGACAATATATTGTAAAGATCCAAA	60
Qy	372	AATAAATGACGCTACGCAAGAACCACTAACTGTACAAACTACACAGCTCATGTTCTG	431
Db	61	AATAAATGACGCTACGCAAGAACCACTAACTGTACAAACTACACAGCTCATGTTCTG	120
Qy	432	TTTCAGCACCCAACATAACTTGTAAAGGATCCAGTGGCAATGAAACACATTACTGG	491
Db	121	TTTCAGCACCCAACATAACTTGTAAAGGATCCAGTGGCAATGAAACACATTACTGG	180
Qy	492	GAACGAAGTGGTTTTCAAGCCATATCTGCCAATGTAAATGGCTATTCTACAA	551
Db	181	GAACGAAGTGGTTTTCAAGCCATATCTGCCAATGTAAATGGCTATTCTACAA	240
Qy	552	AGTGGCAGTCGCATTGTCTCTTTCTTGGATGGTGGAGCAGATCGATTACCTTGG	611
Db	241	AGTGGCAGTCGCATTGTCTCTTTCTTGGATGGTGGAGCAGATCGATTACCTTGG	300
Qy	612	ATACCCTGCTTGGTTGTTAAAGTTTGCAGTGTAGGGTTTGTGGAATTGGAGCCT	671
Db	301	ATACCCTGCTTGGTTGTTAAAGTTTGCAGTGTAGGGTTTGTGGAATTGGAGCCT	360
Qy	672	AATTGATTCATTCTATTCAATGCAGATTGTGGACCTCAGATGGAAGTAGTTACAT	731
Db	361	AATTGATTCATTCTATTCAATGCAGATTGTGGACCTCAGATGGAAGTAGTTACAT	420
Qy	732	TATAGATTACTATGAAACCAGACTTACAAGACTGAGTATTACTAATGAAACATTAGAAA	791
Db	421	TATAGATTACTATGAAACCAGACTTACAAGACTGAGTATTACTAATGAAACATTAGAAA	480
Qy	792	AACGCAATTATATCCATAA	810
Db	481	AACGCAATTATATCCATAA	499

RESULT 9

US-10-025-380-245

; Sequence 245, Application US/10025380
 ; Publication No. US20020182191A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Xu, Jiangchun
 ; APPLICANT: Lodes, Michael J.
 ; APPLICANT: Secrist, Heather
 ; APPLICANT: Benson, Darin R.
 ; APPLICANT: Meagher, Madeleine Joy
 ; APPLICANT: Stolk, John A.
 ; APPLICANT: Wang, Tongtong
 ; APPLICANT: Jiang, Yuqiu
 ; APPLICANT: Smith, Carole L.
 ; APPLICANT: King, Gordon E.
 ; APPLICANT: Wang, Aijun
 ; APPLICANT: Clapper, Jonathan D.
 ; APPLICANT: Skeiky, Yasir A. W.

; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick Thomas S.
; APPLICANT: Carter, Darrick
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.471C14
; CURRENT APPLICATION NUMBER: US/10/025,380
; CURRENT FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 1129
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 245
; LENGTH: 508
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-025-380-245

RESULT 10
US-09-918-995-6918
; Sequence 6918, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; TITLE OF INVENTION: FROM VARIOUS cDNA LIBRARIES
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 6918
; LENGTH: 431
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(431)
; OTHER INFORMATION: n = A,T,C or G

US-09-918-995-6918

Query Match 41.7%; Score 337.4; DB 10; Length 431;
Best Local Similarity 99.7%; Pred. No. 1.5e-95;
Matches 338; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	472	AATGAAACACATTTACTGGAACGAAGTTGGTTTTCAAGCCCATATCTGCCGAAAT	531
Db	1	AATGAAACACATTTACTGGAACGAAGTTGGTTTTCAAGCCCATATCTGCCGAAAT	60
Qy	532	GTAAATGGCTATTCTACAAAGTGGCAGTCGCATTGTCCTTTCTTGGATGGTGGGA	591
Db	61	GTAAATGGCTATTCTACAAAGAGGCAGTCGCATTGTCCTTTCTTGGATGGTGGGA	120
Qy	592	GCAGATCGATTTACCTTGGATACCCTGCTTGGTTAAAGTTTGCACGTAGGG	651
Db	121	GCAGATCGATTTACCTTGGATACCCTGCTTGGTTAAAGTTTGCACGTAGGG	180
Qy	652	TTTGTTGGAATTGGGAGCCTAATTGATTCATTCTATTCAATGCAGATTGGACCT	711
Db	181	TTTGTTGGAATTGGGAGCCTAATTGATTCATTCTATTCAATGCAGATTGGACCT	240
Qy	712	TCAGATGGAAGTAGTTACATTATAGATTACTATGGAACCACTACAAGACTGAGTATT	771
Db	241	TCAGATGGAAGTAGTTACATTATAGATTACTATGGAACCACTACAAGACTGAGTATT	300
Qy	772	ACTAATGAAACATTAGAAAAACGCAATTATATCCATAA	810
Db	301	ACTAATGAAACATTAGAAAAACGCAATTATATCCATAA	339

RESULT 11
US-10-085-783A-36056
; Sequence 36056, Application US/10085783A

; Publication No. US20040037841A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relatiing to Osteoarthritis
; FILE REFERENCE: 4231/2002
; CURRENT APPLICATION NUMBER: US/10/085,783A
; CURRENT FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 36056
; LENGTH: 256
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (2)..(2)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (13)..(13)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (30)..(30)
; OTHER INFORMATION: n is a, c, g, or t

US-10-085-783A-36056

Query Match 12.3%; Score 100; DB 12; Length 256;
Best Local Similarity 99.1%; Pred. No. 8.7e-21;
Matches 111; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 700 ATTGTTGGACCTTCAG-ATGGAAGTAGTTACATTATAGATTACTATGGAACCAGACTTAC 758
Db 14 ATTGTTGGACCTTCAGNATGGAAGTAGTTACATTATAGATTACTATGGAACCAGACTTAC 73

Qy 759 AAGACTGAGTATTACTAATGAAACATTAGAAAAACGCAATTATATCCATAA 810
Db 74 AAGACTGAGTATTACTAATGAAACATTAGAAAAACGCAATTATATCCATAA 125

RESULT 12

US-10-242-535A-36056

; Sequence 36056, Application US/10242535A
; Publication No. US20040013663A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relatiing to Osteoarthritis
; FILE REFERENCE: 4231/2005
; CURRENT APPLICATION NUMBER: US/10/242,535A

; CURRENT FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: US 10/085,783
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
SEQ ID NO 36056
LENGTH: 256
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc_feature
LOCATION: (2)..(2)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (13)..(13)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (30)..(30)
OTHER INFORMATION: n is a, c, g, or t

US-10-242-535A-36056

Query Match 12.3%; Score 100; DB 15; Length 256;
Best Local Similarity 99.1%; Pred. No. 8.7e-21;
Matches 111; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 700 ATTGTTGGACCTTCAG-ATGGAAGTAGTTACATTATAGATTACTATGGAACCAGACTTAC 758
Db 14 ATTGTTGGACCTTCAGNATGGAAGTAGTTACATTATAGATTACTATGGAACCAGACTTAC 73

Qy 759 AAGACTGAGTATTACTAATGAAACATTTAGAAAAACGCAATTATATCCATAA 810
Db 74 AAGACTGAGTATTACTAATGAAACATTTAGAAAAACGCAATTATATCCATAA 125

RESULT 13

US-10-085-783A-48351
; Sequence 48351, Application US/10085783A
; Publication No. US20040037841A1

GENERAL INFORMATION:

; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relatiing to Osteoarthritis
; FILE REFERENCE: 4231/2002
; CURRENT APPLICATION NUMBER: US/10/085,783A
; CURRENT FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12

; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 48351
; LENGTH: 411
; TYPE: DNA
; ORGANISM: Human
US-10-085-783A-48351

Query Match 10.5%; Score 85.4; DB 12; Length 411;
Best Local Similarity 98.9%; Pred. No. 4.8e-16;
Matches 86; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 724 AGTTACATTATAGATTACTATGGAACCAGACTTACAAGACTGAGTATTACTAATGAAACA 783
|||
Db 1 AGTTACATTATAGATTACTATGGAACCAGACTTACAAGACTGAGTATTACTAATGAAACA 60

Qy 784 TTTAGAAAAACGCAATTATATCCATAA 810
|||
Db 61 TTTAGAAAAACGCAGTTATATCCATAA 87

RESULT 14

US-10-242-535A-48351

; Sequence 48351, Application US/10242535A
; Publication No. US20040013663A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2005
; CURRENT APPLICATION NUMBER: US/10/242,535A
; CURRENT FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: US 10/085,783
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 48351
; LENGTH: 411
; TYPE: DNA
; ORGANISM: Human
US-10-242-535A-48351

Query Match 10.5%; Score 85.4; DB 15; Length 411;
Best Local Similarity 98.9%; Pred. No. 4.8e-16;
Matches 86; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 724 AGTTACATTATAGATTACTATGGAACCAGACTTACAAGACTGAGTATTACTAATGAAACA 783
|||
Db 1 AGTTACATTATAGATTACTATGGAACCAGACTTACAAGACTGAGTATTACTAATGAAACA 60

Qy	784	TTTAGAAAAACGCAATTATATCCATAA	810
Db	61	TTTAGAAAAACGCAGTTATATCCATAA	87

RESULT 15

US-10-085-783A-16414

; Sequence 16414, Application US/10085783A

; Publication No. US20040037841A1

GENERAL INFORMATION

APPLICANT: ChondroGene Inc.

APPLICANT: Liew, C.C.

: TITLE OF INVENTION: Combo

FILE REFERENCE: 4231/2002

CURRENT APPLICATION NUMBER: US/1

CURRENT FILING DATE: 2002-02-28

PRIVACY ACT STATEMENT
PRIVACY ACT STATEMENT

PRIORITY FILING DATE: 2001-07-13

PRIOR APPLICATION NUMBER: US 60/2

PRIOR ATTACHMENT NUMBER: 05-001
PRIOR FILING DATE: 2001-03-12

PRIOR APPLICATION NUMBER: US 60/271,955

PRIOR APPLICATION NUMBER: 35
PRIOR FILING DATE: 2001-02-28

PRIVILEGED
NUMBER OF SEQ ID NOS: 58994

; NUMBER OF SEQ
; SOFTWARE: Pate

; SOFTWARE. If
; SEO ID NO. 164

; LENGTH: 13

LENGTH: 125
TYPE: DNA

TYPE: DNA
ORGANISM: Human

Query Match 9.8%; Score 79; DB 12; Length 129;
Best Local Similarity 89.5%; Pred. No. 2.3e-14;
Matches 85; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Search completed: March 4, 2004, 10:22:21
Job time : 351 secs